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Result
No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
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length: 2000000000
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(without alignments)
1830.070 Million cell updates/sec
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.
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// SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:
// SIDS2/gcgdata/geneseq/geneseqp-emb1/AA198.DAT:
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// SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-embl
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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19
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                                               AAW06130
AAR88397
AAW46449
AAW67034
AAW67579
AAW675222
AAB45512
                                                                                                                                                                                                   AAR11896
                                                                                                                                                                                                                                                                                                             SUMMARIES
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Immunogenic conjug
Tetanus toxoid pro
T-cell antigen Tr3
Broad range helper
Tetanus toxin frag
T-cell epitope pep
Tetanus toxoid epi
Tetanus toxin T ce
Tetanus toxin T ce
Foreign epitope P3
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AARI	بر <u>د</u>	0.0	•	112
AAR142	11			112
2 AAG63513 2 AAR14263	- 2	6.9	100.0	112
AAG63	2		•	112
9	22	51	•	112
	N			112
	23	50		112
	N	44		112
AAB4619	2		100.0	112
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2 AAB46177	N I	4.		112
	. N		100.0	113
2 AAG63662	אנ	3 G	100.0	112
	N	4	٠	112
	2	33	•	112
	15	32	•	112
	2	31	•	112
	21	31	•	112
	21	31	•	112
2 AAB46176	2	28	100.0	112
	N.	21	•	112
	N	21		112
	N	21	•	112
	2	21	٠	112
	N	21	•	112
AAB6195	2	21		112
	Ŋ	21	٠	112
2 AAB85702	Ŋ	21	100.0	112
	N	21		
AAY4926	2	21		112
1 AAY84428	N	21	100.0	112

ALIGNMENTS

RESULT 1
AAR11896
ID AAR1
XX
AC AAR1
XX

AAR11896;

19-JUL-1991 (first entry)

Tetanus toxin.

Malaria vaccine; major histocompatibility complex

Immunogenic conjugate constituent peptide,

TT3.

- AAR11896 standard; peptide; 21

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FH Key
FT Peptide
FT P
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Length

21;

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RESULT 2
AAW06130
ID AAW0
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Best Local S
Matches 21
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                                A helper T-cell epitope (AAW06130) comprises amino acids 947-967 of tetanus toxoid protein. It can be utilised in novel peptide vaccines (see also AAW06129, AAW06132) also including B-cell epitope(s) from human or rabbit cholesteryl ester transfer protein (CETP) to elicit an immune response against endogenous CETP activity, thereby treating or preventing a cardiovascular
Sequence
                                                                                                                                                            Cholesteryl ester transfer protein B cell epitope linked to T cell epitope - used to generate vaccine to regulate CETP activity for decreasing the risk of developing a cardiovascular disease e.g.
                                                                                                                                                                                                                                                                                             01-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholesteryl ester transfer protein; CETP; antigen; vaccine; cardiovascular disease; atherosclerosis; tetanus toxoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                          Rittershaus CW,
                                                                                                                                                                                                                                                                                                                     01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                07-NOV-1996
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                                                                                                                                                                                                                                                                     (TCEL-) T CELL
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                                                                                                                                                                                                                   1996-506103/50
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                         such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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 8
                        as atherosclerosis
                                                                                                                           43;
                                                                                                                                                                                                                                                                   SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein T-cell epitope
                                                                                                                                                                                                                                                                                             95US-0432483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
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Pred. No. 3.9e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
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RESULT 4
AAW46449
ID AAW4

AAW46449 standard;

Peptide;

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AAW46449

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RESULT 3
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Matches 21
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                                                                                                                                 This T-cell antigen TT3 peptide may be attached to a core peptide contained in one of the 2 subunits of an alpha-helical coiled-coil heterodimer. Each core peptide is comprised of terminal and internal AA repeat sequences. This peptide antigen is attached to the core peptide through covalent linkages to certain AA of the internal repeats. The 2 subunits of the heterodimer are arranged in a stable alpha-helical coiled-coil configuration having a 1:1 stoichlometry, and the peptide antigen is disposed toward the outer surfaces of the configuration. The heterodimer may be used as a
                                                                                                                                                                                                                                                                          Hetero:dimeric polypeptide immunogen in c with different antigens on each sub:unit for antibody prodn.
                                                                                                                                                                                                                                                                                                                                               Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-antigen; vaccine; alpha-helix; coiled
                                                                                        Sequence
                                                                                                                          synthetic vaccine (optionally multivalent)
                                                                                                                                                                                                                                                    Claim 7; Page 62; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell antigen
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                                                                                                                                                                                                                                                                                                                        WPI; 1996-010880/01
                                                                                                                                                                                                                                                                                                                                                        Cachia PJ,
                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1994;
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                                                       Local
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FNNFTVSFWLRVPKVSASHLE
                   FNNFTVSFWLRVPKVSASHLE
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                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccine; antibody; T-cell; T-lymphocyte;
coiled-coil heterodimer; core peptide; subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 112; DB 17; 100.0%; Pred. No. 3.9e-12; tive 0; Mismatches 0;
                                                       100
                                                                  100
                                                                                                                                                                                                                                                                                                                                                          Houston ME,
                                                      .0%;
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                          Score 112; DB 17;
Pred. No. 3.9e-12;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                           Irvin
                                                                                                                                                                                                                                                                                      coiled-coil configuration
t - useful in vaccines and
                                                                                                                                                                                                                                                                                                                                                          RT,
                                                                                                                         or to generate
                                                                                                                                                                                                                                                                                                                                                          Kay CM;
                                                                Length
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                                                                   21;
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                                           Gaps
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Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA plasmid-based vaccine encodes CETP B cell and helper T cell epitope(s) - used for elevating high density lipoprotein levels, for treating cardiovascular disease
             Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate; dendrimeric poly-lysine; epitope; tumour.
                                                            Tetanus toxin fragment (residues 947-967).
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholesteryl ester transfer protein; CETP; cholesteryl ester; high density lipoprotein; HDL; very low density lipoprotein; VLDL; low density lipoprotein; LDL; T cell epitope; antibody; DNA plasmid-based vaccine; broad range helper T cell epitope;
                                                                                                15-DEC-1998
                                                                                                                                                           AAW67034 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 44; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-549731/50
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01-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broad range helper T cell epitope from the tetanus toxoid protein.
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                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                           FNNFTVSFWLRVPKVSASHLE
                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                              (first entry)
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96US-0640713.
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                                                                                                                                                                                                                                                                                                        100.0%; Score 112; DB 18; 100.0%; Pred. No. 3.9e-12; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      Length
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RESULT 6
AAW67579
ID AAW6
XX
AC AAW6
XC AAW6
XX
DT 02-M
XX
Chim
KW immu
XX
Chim
KW immu
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Synt
XX
PN US58
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PD 01-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis kit are used to provide pharmaceutical compositions and vaccines against tumours. These can be used to support an immune response against viral infections caused by hepatitis virus, HIV or cytomegalo virus. They can be used to enhance immune responses, especially B- and T-cell responses, of humans and animals against bacterial infections. The carbohydrate peptide conjugate stimulates the antibody and T-cell response without stimulating undesired immune responses. The composition is capable of increasing the survival of tumour bearing humans and animals. The present sequence corresponds to residues 947-967 of tetanus toxin. The synthetic peptide corresponding to this sequence may be used as an epitope in a carbohydrate peptide conjugate.
              02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an antibody purified from biological fluid or cells of organisms administered with the carbohydrate peptide conjugate, and (2) a diagnosis kit comprising antigen-specific antibodies elicited by immunisation with the carbohydrate peptide conjugate, antibody and
                                             01-DEC-1998
                                                                          US5843464-A
                                                                                                        Synthetic
                                                                                                                                  Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
                                                                                                                                                                               T-cell epitope peptide #5 for chimeric fimbrin/T-cell epitope peptide
                                                                                                                                                                                                                 02-MAR-1999
                                                                                                                                                                                                                                                 AAW67579;
                                                                                                                                                                                                                                                                            AAW67579 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carbohydrate peptide conjugate used as vaccine - comprises with dendrimeric poly-lysine enabling multiple epitopes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bay S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            covalently attached
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                      FNNFTVSFWLRVPKVSASHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
              95US-0460502.
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                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112; DB 19;
Pred. No. 3.9e-12;
; Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused via a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a T-cell epitope peptide used to generate the chimeric peptide.
 This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal groups of the characterised by overexpression of HER 2/neu or epidermal groups.
                                                                                                           a target
                                                                                                                      Specific killing of tumour cells - using comprising an anti-Fc receptor antibody a
                                                                                                                                                                                                                                         07-JUN-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                  Multispecific single chain antibody; antibody H22; tumour cell; therapy; antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic chimeric fimbrin peptide - useful for vaccination against non-typable Haemophilus influenzae
                                                                                Example
                                                                                                                                                              WPI; 1999-023374/02.
                                                                                                                                                                                         Deo YM,
                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                            17-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                       epidermal growth factor receptor; breast cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetanus toxoid epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW73222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW73222 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bakaletz LO,
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                                                                                                                                                                                                                  MEDAREX INC.
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                                                                                                                                                                                       Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNNFTVSFWLRVPKVSASHLE 21
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                                                                                Column
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ilarity 100.0%;
Conservative (
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95US-0484172
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                                                                             27; 57pp; English.
                                                                                                                                                                                         Graziano
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                                                                                                                                                                                         Somasundaram
                                                                                                                      g a multi-specific molecule and a portion which binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
3.9e-12;
es 0;
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epidermal growth
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FNNFTVSFWLRVPKVSASHLE

Query Match Best Local Matches 2

Similarity

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Length Indels

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ARB45512
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                                                                                The present invention is concerned with methods of treating asthma, eosinophilia, allergic rhinitis and other allergic diseases. These involve the use of interleukin-5 (IL-5) analogues and modified IL-5 proteins and their coding sequences to down-regulate IL-5 activity and thus reduce eosinophil numbers. The allergic diseases may be treated using autovaccines, nucleic acid vaccines or live vaccines. In additional possible that they may be used in the treatment of cancer and it is possible that they may be used in the treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER Z/neu; and (c) a portion which binds to BGFR. The method can be used for treating cancers especially breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infection
   Sequence
                                                                                                                                                                                                                                                                                                                       Example 6; Page 137; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Down-regulating interleukin 5 (IL-5) activity in humans by administering IL-5 and/or an IL-5 analogue, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-2000; 2000WO-DK00205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asthma;
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                                                          helminthic infections
                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis or amelioration of asthma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-672791/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1999;
06-MAY-1999;
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eosinophilia; vaccine; allergic rhinitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
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99US-0132811.
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Pred. No. 3.9e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment,
                                                                                                                  In addition,
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                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                    The present sequence is a tetanus toxin T cell epitope known as Helper Peptide P30. Hybrids of this peptide and an immunogenic peptide derived from tumour rejection antigen precursor MAGE-10 were used to generate polyclonal antiserum against MAGE-10. MAGE-10 binding monoclonal antibodies can be used to detect MAGE-10 expression. A correlation between MAGE-10 expression and cancer has been discovered and thus by determining the presence of MAGE-10, the presence of cancer can be determined. MAGE-10 expression can be detected using an immunoassay, an oligonucleotide hybridisation assay or via other standard techniques. This method is especially useful for determining the presence of bladder, ossophageal, head and neck, prostate or lung cancer, or malancer.
                                           AAY92626;
                                                                                                                                                                                                                                                                  Sequence
              10-AUG-2000
                                                                       AAY92626 standard; Protein; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining presence of cancer in samples, especially useful for detecting bladder, prostate and lung cancer comprises assaying sample for expression of tumor rejection antigen precursor MAGE-10 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; MAGE-10; tumour rejection antigen precursor; bladder cancer; prostate cancer; lung cancer; cancer detection; oesophageal cancer; head and neck cancer; melanoma; myeloma; sarcoma; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; Page 14; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-451624/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY99876 standard; Protein; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetanus toxin T cell epitope helper peptide P30
                                                                                                                                                                                                       21;
                                                                                                                                                                            μ
                                                                                                                                                                         FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FINITUSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                               myeloma
                                                                                                                                                                                                                                                                  21 AA;
                                                                                                                                                                                                        Conservative
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0183714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US24258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brasseur F,
                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                   Score 112; DB 21;
Pred. No. 3.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rimoldi D,
                                                                         ₹
                                                                                                                                               21
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deplaen E;
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                        CC immunogenic cell-associated peptide antigens (PA) such as those CC associated with cancers (i.e. self-proteins), for example, human CC prostate specific membrane antigen (PA), heregulin 2 (Her2) and/or CC fibroblast growth factor 8b (FGF8b). The method comprises effecting CC simultaneous presentation by antigen producing cells (APCs) of the CC animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) CC group derived from the PA and/or at least 1 First T helper cell group which is CC foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and CC predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed. CC The method is used to treat prostate, prostate/breast or breast cancer covered to the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; tetanus toxoid P30 epitope.
                                                                                       Amino acid sequence of the tetanus toxoid P30 epitope.
                                                                                                                        25-JUL-2000
                                                                                                                                                      AAY84428;
                                                                                                                                                                                   AAY84428 standard; Peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The claims detail a method for inducing immune responses against weakly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steinaa L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2; Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 214; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-1998;
20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA09461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-349917/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gautam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200020027-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foreign epitope P30
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                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                       1 FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                           FNNFTVSFWLRVPKVSASHLE
                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouritsen S, Nio
Birk P, Karlsson
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                       (first entry)
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98US-0105011.
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                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                    Score 112; DB 21;
Pred. No. 3.9e-12;
                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor associated prostate cancer
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                                                                                                                                                                                                                                                                                                                    <u>,,</u>
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                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                 AAY49260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the tetanus toxoid P30 epitope. It is cused to create a fusion protein with murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose consensation of the tumour necrosis can be protein. The OPGL protein is synthesised as a type II complete the protein. The murine and human OPGL polypeptides are 87% to homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of CG differentiation in the absence of CSF-1. OPGL is also an activator of CG down-regulation of OPGL activity in an animal. The method comprises compined to induce an immune response in the animal. The method cone CG OPGL nanlogue to induce an immune response in the animal. The method cone conditions characterised by excessive constepprosis or other diseases or conditions characterised by excessive
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 21
 27-APR-1908;
                          27-APR-1999;
                                                     04-NOV-1999.
                                                                                  WO9955730-A2
                                                                                                                                      Carrier protein; CD4+; T cell epitope; encapsulated bacteria.
                                                                                                                                                                              CD4+ T cell epitope P30TT fragment.
                                                                                                                                                                                                             07-FEB-2000
                                                                                                                                                                                                                                        AAY49260;
                                                                                                                                                                                                                                                                  AAY49260 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 106; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-271444/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEBI-) M & E BIOTECH AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200015807-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resorption.
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                                                                                                                                                                                                                                                                                                                                                                  1 FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 100.
21; Conservative
                                                                                                                                                                                                                                                                                                                                      FNNFTVSFWLRVPKVSASHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98DK-0001164.
98US-0102896.
98GB-0008932
                          99WO-IB00844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-DK00481
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 112; DB 21; 100.0%; Pred. No. 3.9e-12;
                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                N6; N10; N19; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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RESULT 13
AAE11764
ID AAE11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides carrier proteins comprising at least 5 CD4+ T cell epitope. The carrier protein comprises at least 1 of N6, N10 or N19. The carrier protein can be prepared by expressing a vector comprising a nucleic acid molecule encoding the protein, in a host cell and recovering the expressed protein. The carrier protein can also be produced by (a) constructing oligonucleotide molecules that encode peptide epitopes; (b) annealing the oligonucleotides to form duplexes; (c) introducing the duplexes into an expression vector; (d) introducing the expression vector into a host cell; and (e) isolating the fusion protein produced from a culture of the host cells. The carrier protein can be used as a protective immunogen in the control of diseases caused by encapsulated bacteria. Sequences AAY49256-266 represent CD4+ T cell epitopes inserted in the recombinant polyepitope carrier proteins.
In vivo down-regulation of amyloid protein for the treatment of Alzheimer's, comprises presenting an amyloidogenic polypeptide
                                                   N-PSDB; AAD18756
                                                                                                    Birk
                                                                                                                                                            21-FEB-2000; 2000DK-0000265
01-MAR-2000; 2000US-186295P
                                                                                                                                                                                                                                              30-AUG-2001.
                                                                                                                                                                                                                                                                                                          Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease; antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS; amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carrier proteins containing CD4+ epitopes useful for protecting against diseases caused by encapsulated bacteria -
                                                                                                                                                                                                             19-FEB-2001; 2001WO-DK00113
                                                                                                                                                                                                                                                                            WO200162284-A2.
                                                                                                                                                                                                                                                                                                                                         Huntington's disease; fronto-temporal dementia; P30 epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium tetani P30 epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE11764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE11764 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 36; 76pp; English.
                                                                                                                                  (MEBI-)
                                                                                                                                                                                                                                                                                                                                                                                                   Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                  2001-589796/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FNNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                               Jensen MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNFTVSFWLRVPKVSASHLE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 112; DB 21; 100.0%; Pred. No. 3.9e-12; o. Mismatches 0;
                                                                                                Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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or

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RESULT 14
AAB85702
ID AAB85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for in vivo down-regulation of amyloid CC protein such as beta amyloid (Abeta) in an animal, including human. The method comprising presenting to the animal's immune system an cCC immunogenically effective amount of at least one amyloidogenic protein CC or its subsequence and/or at least one analogue of the amyloidogenic CC polypeptide. The amyloidogenic protein or its subsequence, and its canalogue is useful for the preparation of an immunogenic composition cc analogue is useful for the preparation of an immunogenic composition cc analogue is useful in the treatment, prophylaxis or amelioration of Alzheimer's CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's CC disease or other diseases characterised by amyloid deposits. They are also useful in the treatment of systemic amyloidosis, maturity onset CC disease or other diseases thuntington's disease, fronto-temporal CC dementia, amyotrophic lateral sclerosis (ALS), pick's disease and CC useful for inducing production of antibodies against an amyloidogenic consplication in the present sequence is Clostridium tetani P30 epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
                                                          Example 1;
                                                                                                                                                                    WPI; 2001-514557/56
                                                                                                                                                                                                                                                              31-JAN-2000; 2000US-0179213
                                                                                                                                                                                                                                                                                             29-JAN-2001; 2001WO-US02937
                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                     Multivalent protein; immune response; Plasmodium vivax; parasite; protozoacide; vaccine; malaria; recombinant; ViVac1; ViVac2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB85702 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                 (USSH ) US
                                                                                                                                                                                                                                                                                                                                                           WO200155181-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of P30 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subsequence
polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related to
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                                                                                                                                                                                                                                 DEPT HEALTH & HUMAN SERVICES
                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or at least one analogue
to the immune system -
                                                                                                                                                                                                ۲
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                                                         25; 59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112; DB 22;
Pred. No. 3.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant; ViVac1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the amyloidogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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The invention relates to recombinant multivalent proteins (I) that stimulate an immune response to Plasmodium vivax. (I) comprises an determinants, fragments or conservative substitutions, derived from

derived from

antigenic

The invention relates to a new method for inducing killing of a tumor cell which expresses HER 2/neu or epidermal growth factor receptor (EGFR). The method comprises contacting the tumor cell with a multispecific protein comprising a component, preferably an antibody, which binds to an Fc receptor (FcR), Her 2/neu or EGFR. The method is useful for inducing killing of a tumor cell from breast cancer, sarcon

Sarcoma

Example 7;

Column 29;

57pp; English

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RESULT 15
AABB5453
ID AABB5453
XX AABB5453
XX AABB5
XX AABB5
XX Directory
Compatible
Compatible
ACC AABB5
XX HER 2
XX PC re
XX PC re
XX PC re
XX PC re
XX Inductory
PR 07-AU
XX O7-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
                                                                                                                                                                                                                                        Inducing killing of tumor cells which expresses HER 2/neu or epidermal growth factor receptor (EGFR) by contacting the cell with multispecific proteins comprising an anti-Fc receptor, -Her 2/neu or -EGFR antibody, useful for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fc receptor; FCR; tumor cell; breast; cancer; sarcoma; carcinoma; HIV; pathogenic; Toxoplasma gondii; candidiasis; systemic lupus; cytostatic; immune thrombocytopenia purpura; immunosuppressive; antiviral; antiprotozoal; tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deo YM,
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07-JUN-1995;
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Pred. No. 3.9e-12;
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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  Score
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Tetanus toxin frag
Universal helper T
T-Helper epitope f
T-cell epitope pep
T-cell epitope pep
Tetanus toxoid epi
Tetanus P2 epitope
Tetanus toxoid T c
                                                                                                                                                                                                                           Description
                                                                                                                                                                 Tetanus toxin epit
Universal T-cell e
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ALIGNMENTS

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PD: 25-JUL-1990:

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PP 27-DEC-1989;

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PR 16-NOV-1989;

PR 17-JAN-1989;

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(ENIE ) ENIR:

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PI Pessi A, Bia
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                                 Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used as universal carriers for prepn. of immunogenic conjugate(s) for
                                                                                                                                                                                     WPI; 1990-225582/30
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17-JAN-1989;
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89IT-0019110
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CC through a linker to a solid phase, forming a complex of (A)-solid phase.

CC where (A) comprises 10-50 amino acids capable of forming a secondary complex of (A)-solid phase.

CC where (A) comprises 10-50 amino acids capable of forming a secondary complex of forming a secondary complex complex comprises an immunogenic substance and/or an immune mediator coupled on (A). The present sequence complex can be used as a scaffold for the production of chase complex can be used as a scaffold for the production of chasolid phase complex can be used as a scaffold for the production of chasolid phase complex can be used as a scaffold for production of complex can be used for the production of complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. (A) derivatised with one or more peptides having fibronection, laminin- or vitronectin-like complastic surfaces, in particular to inhibit tumour growth and metastasis and for promotion of wound healing. Also a derivatised (A) can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                 Non-dendritic peptide carrier linked to a solid phase - useful as diagnostic agent and as a scaffold for production of chemical
                                                                                                                                                                                                                                                                                                   Example 20; Page 124; 262pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-512645/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Universal T-cell epitope peptide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1997.
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Pred. No. 3.9e-07;
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QYIKANSKFIGITEL 15

QYIKANSKFIGITEL

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RESULT 3
AAW11505
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     Matches
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Best Local
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Best Local
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                                                                                                tetanus toxoid, designated TT830, was fused to the 3'-end of DNA encoding heavy chain sequences from the humanised anti-Fc gamma RI monoclonal antibody H22. The resulting fusion protein was shown to be significantly more efficient in antigen presentation and T cell stimulation that the TT830 epitope alone. A similar fusion construct was prepared coding for a mutant, antagonistic form of the epitope (designated TT833S) fused to the anti-Fc gamma RI. The
                                                    Sequence
                                                                                                                                                                                                                                            Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific; fusion protein; chimera; tetanus toxoid; helper T cell epitope; antigen presentation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for the selection of specifically-binding aptamers or as a diagnostic agent. Such diagnostic-(A) molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an infectious, autoimmune or cancerous disease.
                                                                                                                                                                                             Synthetic DNA coding for the wild-type universal Th
                                                                                                                                                                                                                       Example 7; Fig 24; 115pp; English.
                                                                                                                                                                                                                                                                                                     WPI; 1997-052242/05
N-PSDB; AAT58127.
                                                                                                                                                                                                                                                                                                                                         Deo YM,
                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetanus toxoid universal Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW11505
                                                                              inhibiting T cell activation.
                                                                                         Fab22-TT833S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infectious, autoimmune
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15; Conserv
                Similarity
                                                                                                                                                                                                                                                                                                                                         Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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100.0%;
ilarity 100.0%;
Conservative 0
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 Score 74; DE
Pred. No. 3.9
D; Mismatches
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Pred. No. 3.9e-07;
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             3.9e-07
                           DB 18;
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Gaps
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RESULT 5
AAW71321
ID AAW7
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AC AAW7
XX
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AAW67033
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                                                                                                                                                    S
                                                                                                                                                                                                                                                     The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrineric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an CC antibody purified from biological fluid or cells of organisms CC administered with the carbohydrate peptide conjugate, and (2) a diagnosis kit comprising antigen-specific antibodies elicited by immunisation with CC the carbohydrate peptide conjugate. Antibody and CC vaccines against tumours. These can be used to support an immune response CC against viral infections caused by hepatitic virus, HIV or cytomegalo CC virus. They can be used to enhance immune responses, especially B- and T-CC responses, of humans and animals against bacterial infections. The CC carbohydrate peptide conjugate stimulates the antibody and T-cell response without stimulating undesired immune responses. The composition CC is capable of increasing the survival of tumour bearing humans and CC animals. The present sequence corresponds to residues 830-844 of tetanus CC coxin. The synthetic peptide corresponds to this sequence may be used to as an epitope in a carbohydrate peptide conjugate.
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                AAW71321;
                                            AAW71321 standard;
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 13; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with dendrimeric poly-lysine enabling covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carbohydrate peptide conjugate used as vaccine - comprises with dendrimeric poly-lysine enabling multiple epitopes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium tetani.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate; dendrimeric poly-lysine; epitope; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW67033;
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                                                                                                                                           QYIKANSKFIGITEL
                                                                                                                           QYIKANSKFIGITEL
                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-EP01922.
                                            peptide; 15
                                                                                                                                                                                                   100.0%; Score 74;
100.0%; Pred. No.
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                                                                                                                           15
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                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                3.9e-07;
                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                Length 15;
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RESULT 6
AAY04051
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW71321-22 represent universal helper T-cell epitopes derived from tetanus toxin. They are used to enhance host immune response to vaccines. The specification describes a plasmodium yoelii liver stage 17 kDa hepatic and erythrocytic stage protein designated PyHEP17. This protein elicits a response from an 1g1 monoclonal antibody designated Navy Yoelii Liver Stage 3 (NYLS3). This antibody does not recognise sporozoites, but does recognise P. yoelii liver stage parasites. NYLS3 eliminates upto 90% of liver stage parasites. The specification describes a vaccine for reducing the severity or incidence of infection by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises exon 1 and part of exon 2 of the PyHEP17 gene.
                                                      Covalently reactive antigen analog; CRAA; catalytic antibody; electrophilic reaction centre; phosphonate; boronate; vaccine transition state analog; TSA; isostere; gp120; HIV-1; T-helpetetanus; toxoid; B-T-epitope.
                           Clostridium tetani.
                                                                                                                                 T-Helper epitope from tetanus toxoid
                                                                                                                                                                   04-JAN-2000
                                                                                                                                                                                                AAY04051;
                                                                                                                                                                                                                           AAY04051 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 12; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine for protecting mammal against infection by malaria caused by Plasmodium species - comprises a first nucleic acid encoding a first polypeptide capable of eliciting an immune reaction against an antigen expressed during the liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3; hepatic and erythrocytic stage protein; PyHEP17; vaccine; malaria parasite; teanus toxin; P2; helper T-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-541794/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charoenvit Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Universal helper T-cell epitope P2 derived from tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USNA ) US SEC OF NAVY.
                                                                                                                                                                                                                                                                                                                                                                   l Similarity
                                                                                                                                                                                                                                                                                                                             QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                        OY I KANSKFIGITEL
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 19;
Pred. No. 3.9e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoffman
                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA vaccine comprises
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WO9948925-A1

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RESULT 7

AAW67578

ID AAW6

XX AAW6

AC AAW6

XX AAW6

XX Chim

KW Chim

KW immu

XX Synt

XX Synt

XX O1-L

XX O2-J

XX O2-J

XX (OH)

PA (OH)

XX (OH)
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  electrophilic reaction centre, preferably a phosphonate or boronate moiety. Depending on the identity of the epitope, the CRAA may be used to stimulate production of catalytic antibodies specific for predetermined antigens associated with particular medical disorders. They may also be used to permanently inactivate endogenously produced transpared to antibodies produced in certain autoimmune diseases as well as in certain lymphoproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of formula X1-Y-E-X2, in which at the profession, Y is a positively of an epitope of a disease-associated protein, Y is a positively charged amino acid residue, preferably Lys or Arg, and E is an charged amino acid residue, preferably a phosphonate or boron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amongst the specifically exemplified CRAAs is one based on residues 421-436 of a B-cell epitope of gpl20 (see AAR94046) which may be used to counter HIV-1 infections. When used as an immunogen, preferably this CRAA is conjugated at its N-terminal to a T-helper epitope from tetanus toxoid. The present sequence represents the T-helper epitope and corresponds to residues 830-844 of the toxoid.
                                                                                                               01-DEC-1998
                                                                                                                                                                                                                            Chimeric;
                                                                                                                                                                                                                                                         T-cell epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New covalently reactive antigen analogs used for treating e.g. autoimmune diseases, lymphoproliferative disorders, cancers, microbial infections, ischemic and reperfusion injury or septic shock -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paul
                 (OHIS ) UNIV OHIO STATE
                                              02 . TUN-1995;
                                                                              02-JUN-1995;
                                                                                                                                             US5843464-A
                                                                                                                                                                                                           immunogenic
                                                                                                                                                                                                                                                                                             02-MAR-1999
                                                                                                                                                                                                                                                                                                                            AAW67578
                                                                                                                                                                                                                                                                                                                                                          AAW67578 standard; peptide; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patent discloses new covalently reactive antigen analogs (CRAA)
formula X1-Y-E-X2, in which X1 and X2 represent peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                           QYIKANSKFIGITEL 15
                                                                                                                                                                                                                            non-typable Haemophilus influenzae; fimbrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 86; 158pp; English
                                                                                                                                                                                                             composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
llarity 100.0%;
Conservative C
                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                       peptide #4 for chimeric fimbrin/T-cell epitope peptide
                                               95US-0460502
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                                                                              95US-0460502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith
                                                                                                                                                                                                              immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 20;
Pred. No. 3.9e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         T-cell epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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RESULT 8
AAW73220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal growth factor receptor (EGFR), comprises contacting the tumour cell with a multispecific protein molecule (preferably a single chain antibody) comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which
                                                                                                                                                                         comprising an a target cell
                                                                                                                                                                                                                                                            Deo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multispecific single chain antibody; antibody H22; tumour cell; therapy; antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection; epidermal growth factor receptor; breast cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce in immune response against non-typable Haemophilus influenzae. This sequence represents an example of a T-cell epitope peptide used to generate the chimeric peptide.
                                                                                                                                                                                                  Specific killing of tumour cells - using a multi-specific molecule
                                                                                                                                                                                                                                 WPI; 1999-023374/02.
                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
07.-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW73220 standard; Protein; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic chimeric fimbrin peptide - useful for vaccination against non-typable Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  US5837243-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW73220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the manufacture of a synthetic comprising a non-typable Haemophilus influenzae fimbrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-044514/04
                                                                                                                                                                                                                                                                                     (MEDA-)
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                                                                                                                                             7; Column
                                                                                                                                                                                                                                                                                      MEDAREX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                         Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OYIKANSKFIGITEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                     anti-Fc receptor antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaumaya
                                                                                                                                                                                                                                                                                                                 96US-0661052
95US-0484172
                                                                                                                                                                                                                                                                                                                                                            96US-0661052.
                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                            57pp; English.
                                                                                                                                                                                                                                                            Graziano R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74; DB 20;
Pred. No. 3.9e-07;
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                                                                                                                                                                                     and a portion which binds to
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chimeric peptide is
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RESULT 9
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                                                          Query Match
Best Local
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Best Local
                                                                                                                             The present invention is concerned with methods of treating asthma, eosinophilia, allergic rhinitis and other allergic diseases. These involve the use of interleukin-5 (IL-5) analogues and modified IL-5 proteins and their coding sequences to down-regulate IL-5 activity and thus reduce eosinophil numbers. The allergic diseases may be treated using autovaccines, nucleic acid vaccines or live vaccines. In addition it is possible that they may be used in the treatment of cancer and
                                                                                                                                                                                                                                                                   Down-regulating interleukin 5 (IL-5) activity in humans by administering IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or amelioration of asthma or other chronic allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asthma; cancer;
                                                                                              Sequence
                                                                                                                       helminthic
                                                                                                                                                                                                                                Example 1; Page 137; 172pp; English.
                                                                                                                                                                                                                                                                                                                       WPI; 2000-672791/65
                                                                                                                                                                                                                                                                                                                                                 Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binds to EGFR. The method can be used for treating cancers especially breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infection by a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-2000; 2000WO-DK00205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetanus P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB45511 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                        (MEBI-) M & E BIOTECH AS
                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-5; interleukin-5; allergy; cytokine; helminthic infection eosinophilia; vaccine; allergic rhinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
            QYIKANSKFIGITEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYIKANSKFIGITEL 15
                                                                                              15
                                                                                                                      infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA;
                                            100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                99DK-0000552.
99US-0132811.
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15
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                                            Score 74; DB
Pred. No. 3.9
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74;
Pred. No.
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                                                       DB 21;
3.9e-07;
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3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٥,
                                                                  Length 15;
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                                            Gaps
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                                          0
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                                                                                                                                                                                                            The present invention describes a compound (I) for the prevention and/or CC treatment of allergy. The compound comprises at least one allergen CC antigenic determinant (i) recognised by a B cell or an antibody secreted CC by a B cell of a non-atopic individual and at least one antigenic CC determinant (ii) different from the allergen that triggers T cell CC activation. (I) has antiallergic, antiasthmatic. antinflammatory. CC dermatological and immunosuppressive activities, and can be used in a CC vaccine. (I) may be used in a pharmaceutical or cosmetic medicament to CC treat and/or prevent allergies or a disease of allergic origin, CC especially hypersensitivities. These include rhinitis, sinustis, CC urricaria, gastro-intestinal syndromes associated with the ingestion of CC conditions active during the propersensitivities and/or a mixture of these. The CC associated with the treatment of allergic conditions avoids the need for CC drug treatment, which often causes undesirable side-effects. Also, prior are thrug therefore a summer of allergic conditions are their their causes undesirable side-effects. Also, prior
                                                Query Match
Best Local S
Matches 15
                                                                                                                                                  art drug therapies alleviate symptoms, but do not influence their causes, however (I) actually combats the cause of an allergic reaction. The present sequence represents a peptide, which is used in an example from the present invention
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 30; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound for prevention and treatment of allergies comprises at least one allergen antigenic determinant recognized by a B cell and least one antigenic determinant which does not trigger T cell activation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saint-Remy J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atopic dermatitis; acute urticaria; chronic urticaria; gastro-intestinal syndrome; food allergen; oro-pharyng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T cell epitope;
antiallergic; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY82637 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaphylactic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetanus toxoid T cell epitope peptide SEQ ID NO:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIO ) UCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intiallergic; antiasthmatic; antiinflammatory; dermatological; immunosuppressive; vaccine; rhinitis; sinusitis; bronchial ast
                                                15;
1 QYIKANSKFIGITEL
                                                               Similarity
                                                                                                                  15
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacquemin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98EP-0870167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-BE00092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B cell epitope; allergy; allergen; antigenic;
                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rome; food allergen; oro-pharyngeal syndrome;
drug hypersensitivity; allergic reaction.
            15
                                             0
                                                               Score 74;
Pred. No.
                                                Mismatches
                                                           3.9e-07;
                                                                               DB 21;
                                                                            Length 15;
                                             Indels
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OYIKANSKFIGITEL

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RESULT 12
AAY84427
ID AAY84
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AC AAY64
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Best Local
                                                                                                                                                                                                                                                                                                                                                  The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (i) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the east 1 clast 1 B-cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2; Heregulin 2; Fibroblast growth factors, FGF8b; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cance prostate cancer; cell-associated peptide antigen.
 25-JUL-2000
                              AAY64427;
                                                                                                                                                                                                                                                                                           human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign Thelper epitope (e.g. P2 and/or P30) are also claimed. The method is used to treat prostate, prostate/breast or breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1998;
20-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY92625;
                                                       AAY84427 standard; Peptide; 15
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 213; 220pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinaa L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1999;
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                                                                                                                                                                                                                                                                           the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-349917/30
                                                                                                                                                                                                        Similarity
                                                                                                                                                             QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouritsen S, Niv
Birk P, Karlsson
                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
(first entry)
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98US-0105011.
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                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                     Score 74; DB 21;
Pred. No. 3.9e-07;
                                                          ጅ
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haaning J,
                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer
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                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the tetanus toxoid P2 epitope. It is CC used to create a fusion protein with murine osteoprotegerin ligand CC (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis CC factor receptor family, which blocks osteoclastogenesis in a dose consense the protein. The opgl protein is synthesised as a type II CC transmembrane protein. The murine and human OPGL polypeptides are 87% CC transmembrane protein. The murine and human OPGL polypeptides are 87% CC combined with CSF-1. It is not capable of inducing osteoclast CC combined with CSF-1. It is not capable of inducing osteoclast of CC differentiation in the absence of CSF-1. OPGL is also an activator of CC down-regulation of OPGL activity in an animal. The method comprises CC using at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at least one CC and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 15
              Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; circumsporozoite
                                                                                   Clostridium tetani tetanus toxoid T-cell epitope, P589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                          06-JUN-2000
                                                                                                                                                                                           AAY70300 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; osteoporosis; bone resorption; tetanus toxoid P2 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the tetanus toxoid P2 epitope
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l Similarity 100.0%;
15; Conservative 0
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                                                                                                                                                                                                                                                                                 QYIKANSKFIGITEL
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98US-0102896
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                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 21;
Pred. No. 3.9e-07;
Mismatches 0;
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surface protein-1; MSP-1; MSP-2;
                                                                                                                                                                                                                                                                                                                                                                                    Length 15;
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AAY44763
ID AAY44
XX AAY44
XX AAY44
XX O4-MA
DT 04-MA
XX Surfa
CX Surfa
KW recom
KW antib
KW P2; t
XX AY40
COS Clost
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                                                                                          Surface layer protein; S-layer secretion signal; antibiotic; vaccine; recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff; antibacterial enzyme; surface glycoprotein; T-cell activating epitope; P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), mSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparassitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
                                                               Clostridium tetani
                                                                                                                                                                          Tetanus toxoid protein derived T-cell activating epitope
                                                                                                                                                                                                              04-MAY-2000
                                                                                                                                                                                                                                                                         AAY44763 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Clostridium tetani. It is used in the construction of recombinar protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                  WO200004170-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from retanus toxoid and 21 antigenic epitopes
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is the tetanus
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US DEPT HEALTH & HUMAN
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Pred. No.
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3.9e-07;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conditions so that cleavage occurs at aspartate prolline dispeptide site without solubilising the protein. The cleavage is accomplished while the fusion protein is in an insoluble aggregate form which facilitates for purification of the protein. The method is useful for producing pure purification of the protein. The method is useful for producing pure for proteins including recombinant human and animal therapeutic antibiotic and vaccine peptides, enzymes, protein polymers, and antibacterial for enzymes for foodstuffs.

The present sequence is a T-cell activating epitope P2 derived from tetamus toxoid protein. This sequence was fused to a DNA encoding from tetamus toxoid protein. This sequence was fused to a DNA encoding for finectious pancreatic necrosis virus surface glycoprotein which is a vaccine candidate. This chimeric protein was in turn fused to DNA encoding C. crescentus S-layer protein from amino acid 690 onwards and contains native Asp-Pro site) for construction of a recombinant fusion construct which is expressed in Caulobacter and then cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                            Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine; Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease; antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS; amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy; Huntington's disease; fronto-temporal dementia; P2 epitope.
                                                                                                                 Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                AAE11763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a method for cleaving a recombinant fusion protein which is produced by Caulobacter and consists of Caulobacter surface layer (S-layer) protein (containing the C-terminal secretion signal) and a target protein heterologous to Caulobacter. The cleavage of target protein from the S-layer protein is carried out under mild acid
                                                                                  WO200162284-A2
                                                                                                                                                                                                                                                         Clostridium tetani P2 epitope
                                                                                                                                                                                                                                                                                              18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                               AAE11763 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage of Caulobacter produced recombinant fusion proteins useful for producing vaccine peptides
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15; Conservative
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                                                                                                                                                                                                                                                                                                                                                               peptide;
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Pred. No. 3.9e-07;
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19-FEB-2001; 2001WO-DK00113.

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Search completed: July 22, 2003, 08:08:15 Job time : 2.09218 secs
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                                                                                                                                                                                                                                                                                           The invention relates to a method for in vivo down-regulation of amyloid CC protein such as beta amyloid (Abeta) in an animal, including human. The CC method comprising presenting to the animal's immune system an CC immunogenically effective amount of at least one amyloidogenic protein CC or its subsequence and/or at least one analogue of the amyloidogenic CC polypeptide. The amyloidogenic protein or its subsequence, and its CC analogue is useful for the preparation of an immunogenic composition CC comprising an adjuvant for down-regulating amyloid in an animal. They are CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's CC disease or other diseases characterised by amyloid deposits. They are CC also useful in the treatment of systemic amyloidosis, maturity onset CC disease or other diseases, Huntington's disease, fronto-temporal CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and CC prion-related transmissable spongiform encephalopathies. They are also CC useful for inducing production of antibodies against an amyloidogenic CC polypeptide. The present sequence is Clostridium tetani P2 epitope CC related to the invention.
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In vivo down-regulation of amyloid protein for the treatment of Alzheimer's, comprises presenting an amyloidogenic polypeptide or its subsequence and/or at least one analogue of the amyloidogenic polypeptide to the immune system .
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N-PSDB; AAD18755.
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01-MAR-2000; 2000US-186295P.
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                                                                                                                                                                   100.0%; Score 74; DB 22; Length 15; 100.0%; Pred. No. 3.9e-07; ative 0; Mismatches 0; Indels
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ILPR_BRALA
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INSR_RAT
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INSR_LYMST
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	Q03145 mus musculu P07949 homo sapien P2917 homo sapien P54761 mus musculu P09759 rattus norv Q91571 xenopus lae Q00944 gallus gall Q91736 xenopus lae P54762 homo sapien Q91738 xenopus lae P53356 hydra atten P34152 mus musculu

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> C X C	-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, -I-FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, -I-FUNCTION: ESSENTIAL ON NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF- ALPHA AND AMPHIREGULIN.	MEDLINE=93194196; PubMed=8095488; Ehsani A., Low J., Wallace R.B., Wu A.M.; "Characterization of a new allele of the human ERBB2 gene by allele- specific competition hybridization."; Genomics 15.426-429(1991)	SEQUENCE OF 737-1031 FROM N.A. MEDIJINE=86016729; PubMed=2995967; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Semba K., Kamata Protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma."; Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985). [4]	MEDLINE=86070181; PubMed=2999974; MEDLINE=86070181; PubMed=2999974; Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., MCGrath J., Seeburg P.H., Libermann T.A., Schlessinger J., Francke U., Levinson A., Ullrich A.; "Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene."; Science 230:1112-1139(1985).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. PAGE 11863; PubMed=3003577; Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N., Saito T., Toyoshima K.; "Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor."; Nature 319:230-234(1986).	HER2) (MLN 19). NGL OR NEU. man). Chordata; Craniata; Vertebrata; Euteleostomi; ia; Primates; Catarrhini; Hominidae; Homo.	13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Receptor protein-tyrosine kinase erb8-2 precursor (EC 2.7.1.112) (D185erb82) (NEU prote-oncogene) (C-erb8-2) (Turosine kinase-type (el)	T 1 HUMAN ERB2 HUMAN STANDARD; PRT; 1255 AA.

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InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkïnase.
InterPro; IPR0002174; Furin-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR0021245; Tyr pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
Pfam; PF01030; Recep L domain; 2.
Pfam; PF00757; YLP; 2.
Pfam; PF00751; Furin-like; 1.
SMART; SM00261; EU; 3.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00100; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene farm; Arbo
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EMBL; M11730; AAA75493.1; -
EMBL; M10303; AAA75493.1; -
EMBL; M10303; AAA75493.1; -
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POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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an email to license@isb-sib.ch).
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TISSUE=Neuroblastoma;
K MEDLINE=86118662; PubMed=3945311;
Rargmann C.I., Hung M.-C., Weinberg
                                    Neuron 6:6
[3]
STRUCTURE
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P06494;
01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
 STRUCTURE BY NMR OF 650-668.
MEDLINE=92155181; PubMed=1346763,
Gullick W.J., Bottomley A.C., Lo
                                                                                       MEDLINE=91222560; PubMed=2025425;
Lai C., Lemke G.;
"An extended family of protein-ty-
expressed in the vertebrate nervo
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                     C., Lemke G.;
extended family of protein-tyrosine kinase tressed in the vertebrate nervous system.";
uron 6:691-704(1991).
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newman R., Crumpton M.J., Sternberg M.J.E., Campbe "Three dimensional structure of the transmembrane oncogenic and oncogenic forms of the neu protein." EMBO J. 11:43-48(1992)
  EMBL;
                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTOR:
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOR
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COM-
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF,
ALPHA AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + prote
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                                                     requires a license agreement (So
an email to license@isb-sib.ch).
CAA27059.1; ALT_INIT.
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DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF01030; Recep_L_domain; 2.

Pfam; PF00757; YLP; 2.

DR Pfam; PF00757; YLP; 2.

DR Probom; PP000001; buk_pkinase; 1.

DR SMART; SM00261; FU; 3.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transmembrane; Glycoprotein; Kultigene family; Receptor; Signal; """" Transmembrane; Glycoprotein; kinase; ATP-binding; Phosphorylation; """ Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation; """ Transmembrane; "" Transmembrane; """ Transmembrane; "" Transmembrane; """ Transmembrane; "" Transmembrane; """ Transmembrane; """ Transmembrane; """ Transmembrane; """ Transmembrane; """ Transmembrane; """ Transmembrane
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P; P11362; IFGK.
              ; EGFR_L_domain.
; Euk_pkinase.
; Furin-like.
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Nakamura T., Ushijima T., Ishizaka Y., Nagao M., A
Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syrian hamster neu
Gene 140:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DIN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proto-oncogene) (C-erbB-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q60553;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                        FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
ween the Swiss Institute of Bioinformatics and the EMBL OULSE
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for com
                                                                                       RESIDUES.
SIMILARITY:
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PTM: LIGAND-BINDING IN
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                                           ry is copyright. It is produced through Institute of Bioinformatics and the EM
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Best Local Similarity
Matches 1091; Conser
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Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF001030; Recep_L_domain; 2.
Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF02757; YLP; 2.
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SMART; SM00219; TYrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00110; PROTEIN KINASE DOM; 1.

PROSITE; PS00111; PROTEIN KINASE DOM; 1.

Transmembrane; Glycoprotein; Multigene family; Rece

Transferase; Tyrosine-protein kinase; ATP-binding;
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to license@isb-sib.ch).
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To-INV-2002 (Rel. 41, Last sequence update)
Epidermal growth factor receptor precursor (EC 2)
EGFR OR ERBB1.
HOMO Sanian.
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MEDLINE-84219729; PubMed=6328312;

Ullrich A., Coussens L., Hayfilck J.S., Dull T.J., Gray A., Ta
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.,
"Human epidermal growth factor receptor CDNA sequence and aber
expression of the amplified gene in A431 epidermoid carcinoma
Nature 309:418-425(1984).
    Reiter J.
Lampland
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MEDLINE=95382957;
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Mammalia; Eutheria; Primates;
                                                                                                                                         Maihle N.J.; "Comparative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Possible role of variant RNA transcripts in the regulation "possible role of variant RNA transcripts in the regulation epidermal growth factor receptor expression in human placent Mol. Reprod. Dev. 41:149-156(1995).
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                                                                                                                       mouse alternative
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MEDLINE=21100872;
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"Expression of a truncated epidermal
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kb alternative transcript from the
receptor gene encodes a truncated
receptor 32:4050-4056 (1996).
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    Threadgill D.W., Danielsen., Balasubramaniam S., Cross
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                                                                                                                                                                                                                                                                                                                                         in ovarian cancer.";
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SEQUENCE OF 150-962 FROM N.A.
MEDLINE=84249835; PubMed=6330563;
Xu Y.H., Ishii S., Clark A.J.L., Sulliva
Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maihle N.J.;
"Human and mouse alternative EGFR transcripts encoding only extracellular domain of the receptor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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      Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M Howk R., Givol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (E) receptor and HER2/neu are located in their carboxyl-terminal Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                   Mroczkowski B., Mosig G., Co
"ATP-stimulated interaction
and supercoiled DNA.";
                                                                                                                                                                                                                                                   MEDLINE=85270438; PubMed=2991899; Ishii S., Xu Y.H., Stratton R.H., Roe "Characterization and sequence of the
                                                                                                                                                                                                                                                                                                                                          MEDLINE=91107677; PubMed=1988448; Haley J.D., Waterfield M.D.; "Contributory effects of de novo
                                                                                                                                                                                                                                                                                                                                                                                          Oncogene
[11]
                                                                                                                                                                                                                                                                                                                                                                                                         Waterfield M.D.;
"The human EGF receptor identification of sequer
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Evans R.M., Verma I.M., Gill G.N., Rosente
"Expression cloning of human EGF receptor
amplification and three related messenger
                                                                        PHOSPHORYLATION.
MEDLINE=89278137;
                                                                                                                                                               RECEPTOR ACTIVITY.
                                                                                                                                                                                     Submitted
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-29
                                                                                                                                                                                                                                                                                                           "Contributory effects of de novo transcription and transcript termination in the regulation of human factor receptor proto-oncogene RNA synthesis.";
J. Biol. Chem. 266:1746-1753(1991).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-29
                                                                                                                                                                                                                                                                                                                                                                                                                                             Haley J
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MEDLINE=88217333;
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                                                                                                         309:270-273 (1984)
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use by non-profit institutions as long a
modified and this statement is not removed.
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MEDLINE=98225196; PubMed=9556602;
Abe V., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda

"Disulfide bond structure of human epidermal growth factor re
J. Biol. Chem. 273:11150-11157(1998).
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Smith K.D., Davies M.J., Bailey D., Renouf D.V.,
"Analysis of the glycosylation patterns of the extra control patterns of the extra country fibroblasts.";
Orany fibroblasts.";
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REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.; "Characterization of the N-oligosaccharides attached to the atypical Asn-X-Cys sequence of recombinant human epidermal growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carpenter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87297456; PubMed=3039909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20198209;
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ASN-528.
                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.
FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed in ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alternative splicing.
TISSUE SPECIFICITY: Expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 truncated isoform/TEGFR, 3/p110 and 4; and 4 isoforms; 1/p170 and 4 isoforms; 1/p17
                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                         U48724;
U48725;
U48726;
                                                                                                                                                                                                                X00588;
U95089;
U48722;
U48723;
  14
                                       11
                                                                                                   Similarity
                                 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
LLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN
                                                                                                                                                                                                                                                                                                               equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. 56:881-914(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for epidermal growth factor
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                                                                                                                                                         ; CAA25240.1; -... AAB53063.1; -... AAC50802.1; -... AAC50804.1; -... AAC50796.1; -... AAC50797.1; -... AAC50798.1; -...
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                                                                        46.4%; Sco
49.8%; Pro
ative 176;
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                                                                            Pred. No. 7.8e6; Mismatches
                                                                                                 Score 3158;
Pred. No. 7.
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7.8e-161;
nes 349;
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extracellular domain
in Chinese hamster
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          ATSN--NSTVACIDRNGLOSCPIKEDSFLORYSSDPTGALTEDSIDDTFL---
                                                                                                                                EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-

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EGFR

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Elsinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-i--FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast."
                                                                                                                                                                                                                                   MEDLINE=94170986; PubMed=8125255; Luetteke N.C., Phillips H.K., Qiu Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93126380; PubMed=7678348; Paria B.C., Das S.K., Andrews G.K., Dey S.K.; Earla B.C. Das S.K., Andrews G.K., Dey S.K.; Expression of the epidermal growth factor rein mouse blastocysts during delayed implantat proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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15-JUN-2002
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01-FEB-1996
                                                                                      SEQUENCE
                                                                                                         Oncogene
                                                                                                                             "Comparison of EGF
                                                                                                                                            MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Sch
                                                                                                                                                                             SEQUENCE OF 1-714 FROM N.A.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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ptor tyrosine kinase.";
s Dev. 8:399-413(1994).
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7:1957-1962(1992)
                                                                                                           6:673-676(1991).
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                                                                                                                              Ullrich A., Schlessinger J., Givol receptor sequences as a guide to
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Rodentia;
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InterPro; IPR000719;
InterPro; IPR002174;
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of
synthesis, and cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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303425; AAA17899.1;

359698; CAA42219.1;

L1 L06864; AAA53029.1;

212608; CAA78249.1;
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   CAA55587.1;
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EPIDERWAL GROWTH FACTOR RECEPTOR

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> W (IN REF. 5).
> F (IN REF. 4).
-> DR (IN REF. 6).
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                                                                                                                                                        Plowman G.D., Cuiouscou J.-M., Whitney G.S., Gree Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HERA/p180erbB4, a epidermal growth factor receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
 phorbol ester."
J. Biol. Chem.
                                              Klagsbrun M.;
"A novel juxtamembrane
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                 tissue distribution
                                                                              Elenius K.,
                                                                                           TISSUE=Fetal brain;
MEDLINE=97476287; PubMed=9334263;
                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS JM-A AND
                                                                                                                                                                                                                                     TISSUE=Breast carcinoma;
MEDLINE=93189574; PubMed=8383326;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLV
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                                                                           Corfas G.,
                                                                                                                                                                                                                                                                                                                                                        (Human)
272:26761-26768(1997)
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Primates;
                                              domain isoform
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                            differential processing
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Catarrhini; Hominidae;
                                                                           Choi C.J.,
                                           of HER4/ErbB4. Isoform-specific
                                                                                                                             JM-B)
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ProDom; PD000001; EUK primour,
SMART; SM00261; FU; 4.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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NP BIND
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RECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B; ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED BUT NOT JM-B. SO, THEY RESPECTIVELY REFRESENT CLEAVABLE AND NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.

CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.

TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART, KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM, PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND BRANST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L07868; AAB59446.1; -. HSSP; P11362; IFGK.
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InterPro; IPR004019; YLP_motif.
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2, NRG-3,
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SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH O
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PF00757; Furin-like; 1.
PF01030; Recep L domain;
PF02757; YLP; 2.
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
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G-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND
INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
CTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing.
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         EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYS-RICH.

CYS-RICH.

CYS-RICH.

PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
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RECEPTOR PROTEIN-TYROSINE
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544 CRVLQGLPREYVNARHCLPCHPECQP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPS
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                                                                      ELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                             FINCTKINGNLI
                                                                                                                                                                                                                                                                                                    FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
                                                                                                                                                                                                                                                                                                                                                    V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTVDSSNIDK
                                                                                                                                                                                                                                                                                                                                                                                                LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN
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PHOSPHORYLATION (A)
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Pred. No. 4.4
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TISSUE=Heart;
MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R
                                                                                                                                        TERB4 RAT STANDARD; PRT; 1308 AA. 062956; Q9Z2N7; Created)
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precu
                                                   SEQUENCE FROM
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                               NCBI_TaxID=10116;
                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEE 1069
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                                                                                                                                                                                                                                                                                                         QEYSTKYFYKQNGRIRPIVAENPEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                 ENPFVSRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
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                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PLAP-SEGAGSDVFDGDLGMGAAKGLQS
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                                                                                           Craniata; Ver
Sciurognathi;
      R.R.,
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       Ope1
                                                                                           Vertebrata; l
thi; Muridae;
                                                                                                                                                     precursor
    D.J.,
                                                                                                                                                      (E)
                                                                                           Euteleostomi; Murinae; Rat
                                                                                                                                                     2.7.1.112).
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         A Pfam; PFULL;
A Pfam; PF01030; Kec.,
R Pfam; PF02757; YLP; 2.

DR Pfam; PF02757; YLP; 2.

DR PRINTS; PR001009; TYRKINASE.
DR ProDom; PD000001; Euk pkinase; 1.

SMART; SM00261; FU; 4.

DR SMART; SM00261; FU; 4.

DR PROSITE; PS00101; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00101; PROTEIN KINASE TOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.
    InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR000719; Furin-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWI
                                                                                                                                                                                                                                                                                                                                             EMBL; AF041838; AAD08899.1; -. EMBL; U52531; AAC53051.1; -. HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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25
1308
651
675
1308
                                                                                                                                                                                                                                                                                                                             EGFR_L_domain.
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CYTOPLASMIC

(POTENTIAL)

Receptor; Signal; ing; Phosphorylation.

KINASE

ERBB-4.

S 밁 ર્ В S 밁 S 밁 á 밁 Ś 밁 Ş 멍 Ś 밁 ક 밁 ર્ક 밁 5 밁 á

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STRAIN=Sprague-Dawley; TISSUE-Spinal cord;

MEDLINE=97184212; PubMed=9030624;

Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.;

"Expression of neuregulins and their putative receptors, ErbB2 and ErbB3, is induced during Wallerian degeneration.";

J. Neurosci. 17:1642-1659(1997).

J. NEUROSCI. 17:1659(1997).

NOT ACTIVATED BY BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NOTACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-!- SUBUNIT: HOMODIMER ON HETERODIMER WITH EACH OF THE OTHER ERBB
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Neuregulins promote survival and growth of breats tence of BrbB2 and ErbB4 expression ventricular mycoytes.";
J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An extended family of prote expressed in the vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NEWYOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE REFIICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                              PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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R Pfam; PF00757; Furin-like; 1.

R Pfam; PF00757; Furin-like; 1.

R Pfam; PF01030; Recep L domain; 2.

Pfam; PF01030; Recep L domain; 2.

R PRINTS; PR00109; TYRKINASE; 1.

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R SMART; SM00219; TYRKC; 1.

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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90015140; PubMed=2797166; Wittbrodt J., Adam D., Malitschek B., Mau Telling A., Robertson S.M., Schartl M.; "Novel putative receptor tyrosine kinase inducing Tu locus in Xiphophorus.";
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Eukaryota; Metazoa; Chordata; Craniata; Pertebrata; Euteleos

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprinodontiformes; Poeciliidae; Xiphophorus.
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15-JUN-2002 (Rel.
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SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY
CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSA
                             GRCVASCNILLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCSKSAHFQDGPQCI
                                                  QECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
                                                                                                                   ANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDS
                                                                                                                                                                                                                                                                                                                                   CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS
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                                                                                                   NTINWRRLFRSEDOSIEYDART
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC (c-erbB3) (Tyrosine kinase-type cell surface receptor
                              SEQUENCE FROM N.A.

MEDLINE-90083234; PubMed-2687875;

Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson Yeolation and characterization of ERBB3, a third membe ERBB/epidermal growth factor receptor family: evidence overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                       ERB3
                                                                                                                          NCBI_TaxID=9606;
[1]
                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                   ERBB3 OR HER3
  MEDLINE=9,0311312;
               SEQUENCE FROM
                                                                                                                                                                       Homo sapiens (Human).
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  PubMed=2164210,
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Catarrhini;
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                                                                      Aaronson S.A.;
hird member of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katon M., Tazana I., Cognomerated as well as transmembrane "C-erbB3 gene encodes secreted as well as transmembrane tyrosine kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEGREGULINS AND -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an addition factor receptor related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
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Katoh M., Yazaki Y., Sugimura
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                                                                                                                                                                                                                                                        SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES
AND PROMOTES ITS ASSOCIATION WITH THE PAS SUBUNIT OF
PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).
DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MANMARY TUMORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEM SECRETED (SHORT FORM).
ALTERNATIVE PRODUCTS: TWO FORMS,
                                                                                                                                                                                                                                   DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAM SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate.
SUBUNIT: HETERODIMER WITH
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Y., Sugimura T., odes secreted as
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EMBL; M29366; AAA35790.1; -.
EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB26935.1; -.
PIR; A36223; A36223.
HSSP; P11362; 1FGK.

EMBL; S61933; AAB2695.1; -.
EMBL; S61935; AAB2695.1; -.
HSSP; P11362; IFGK.
Genew; HCNC:4331; ERBB3.
MIM; 190151; -.
InterPro; IPR000144; EGFR L domain.
InterPro; IPR0002174; Furin-like.
InterPro; IPR0002174; Fyr pkinase.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00757; Furin-like; 1.

Pfam; PF00069; pkinase; 1.
Pfam; PF000757; Furin-like; 1.
Pfam; PF01030; Recept_domain; 2.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYrKC; 1.
SMART; SM00219; TYrKC; 1.
PROSITE; PS001107; PROTEIN_KINASE_TYR; FALSE_NIPROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00109; PROTEIN_KINASE_TYR; FALSE_NEG.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; GlycoproteIn; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

Alternative splicing.

SIGNAL 1 19 POTENTIAL.

SIGNAL 1 19 POTENTIAL.

CHAIN 20 1342 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3

DOMAIN 20 643 EXTRACELLULAR (POTENTIAL).

TRANSMEM 644 664 POTENTIAL.

DOMAIN 665 1342 CYTOPLASMIC (POTENTIAL).

DOMAIN 709 966 PROTEIN KINASE.

NP_BIND 715 723 ATP (BY SIMILARITY).

BINDING 742 742 ATP (BY SIMILARITY).

BINDING 742 844 BY SIMILARITY.

DISULFID 186 194 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

DISULFID CARBOHYD CARBOH CA

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CKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEBITGYLYISAWPDSLPDLSVFQ
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                                 NLQVIRGRILHNGAYS-LTLQGLGISWLGIRSLRELGSGLALIHHNTHLCFVHTVPWDQL
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                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
              NCBI_TaxID=10116; [1]
SEQUENCE
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Pfam; PP00069; pkinase; I.
Pfam; PP00757; Furin-like; 1.
Pfam; PP01030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SWART; SW00261; FU; 5.
SWART; SW00219; TYRKC; 1.
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J. Neurosci. 17:1642-1659(1997).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGITING AND IS ACTIVATED BY NEUREGITI
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STRAIN=Sprague-Dawley; TISSUE-SC1
MEDLINE=97184212; PubMed=903624;
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U29339; AAC28498.2;
EMBL; U52530; AAC53050.1;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107;
PROSITE; PS00109;
PROSITE; PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PYM: LICAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
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N.J., Koland
(DEC-2001)
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gue-Dawley; TISSUE=Sciatic
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PROTEIN_KINASE_TYR; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_DOM; 1.
YCoprotein_Multigene family; Rece
ycoprotein_kinase; ATP-binding;
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1 J.G.
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CYTOPLASMIC (POTENTI)

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CRC64; Length

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Indels

155;

Gaps

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9 35

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525

596

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P04412; 061601; 09W2G0; P81B68;

13-AUG-1987 (Rel. 05, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Epidermal growth factor receptor precursor (EC 2.7.1.112) (Egfr)

(Gurken receptor) (Torpedo protein) (Drosophila relative of ERBB).

EGFR OR TOP OR C-ERBB OR DER OR CG10079.

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophiliae; Drosophila.

MCBI_TaxID=7227;
                                                        MEDLINE=94350209; PubMed=8070664; Clifford R., Schupbach T.; "Molecular analysis of the Drosophila EGF that several genetically defined classes subdomains of the receptor protein."; Genetics 137:531-550(1994).
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S.-Y., Katz J.,
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    II, Bilodeau-Wentworth D.;
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-:- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAMAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS. CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE AUTERO-POSTFERIOR AND DORSO-VENTRAL DELEMBRYANIANTION OF BOTH THE EMBRYO, PLAYS A ROLE IN THE ESTRALISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL BURDROCCTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL BURDROCCTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL BURDROCCTODERMAL NERVOUS SYSTEM AND PRODUCTION OF
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.

TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, CENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADDITIS EXPRESSION IS HIGH IN BRAIN CORTEX THE PROFILE OF THE PROPERTY OF THE PROPE
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SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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314:178-180(1985).
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Best Local
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Pfam; PF00757; Fuxin-like; 1.
Pfam; PF01030; Recept_domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00219; TYrKC; 1.
PROSITE; PS00107; PROTEIN KINASE AT
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DOMAIN
DOMAIN
NP BIND
BINDING
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MOD_RES
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PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00119; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.
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HSSP; P11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X78919;
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like
InterPro; IPR001245; Tyr_pkinase.
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LQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP---
                      KEPEOKVWVNENLRADLCEKNGTICSDOCNEDGCWGAGTDOCLTCKNFNFNGTCIADCGY
                                               RNPHOALLHTANRPEDECVGEGLACHOLCARGHCWGPGPTOCVNCSQFLRGQECVEECRV
                                                                       LETIHGRQLMESMFAALAIVKSSLYSLEMRNLKQISSGSVVIQHNRDLCYVSNIRWPAIQ
                                                                                     LQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRBLGSGLALIHHNTHLCFVHTVPWDQLF
                                                                                                                        ILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKBITGYLNIEGTHPQFRNLSYFRN
                                                                                                                                      FLPESFDG--DPASNTA------PLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQN
                                                                                                                                                                         PQDKMDKGGE----CVPCNGPCPKTCPGVTVLH-----AGNIDSFRNCTVIDGNIR
                                                                                                                                                                                                                                        LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                                                                                                                                                                            MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                                                                              YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                                                                                                                                                                                                                                                      RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFIGITELNRSRACHPCSP
                                                                                                                                                                                                                                                                                                                                                                                 YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV-
                                                                                                                                                                                                                                                                                                                                                                                               YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                  KICIGTKSRLSVPSNKEHHYRNLRDRYTNCTYVDGNLKLTWLPNENLDLSFLDNIREVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG
                                                                                                                                                                                                PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA 375
                                                                                                                                                                                                                            KNFFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP
                                                                                                                                                                                                                                                                              SCTHG-
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138 1198

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Pred. No. 2.3e-97;
6; Mismatches 433;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EXTRACELLULAR (POTENTIA
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433;
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ve splicing;
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RESULT 12
ERBB LT ERBB AC P0053
AC 21-JU
DT 15-JU
DT 15-JU
DT 77008
GN V-ERBB
OS Avian
OC Virus
OX NCBI-
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                                            ERBB ALV STANDARD; PRT; 6.
P00534;
21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Tyrosine-protein kinase transforming p
Viruses; Retroid viruses; NCBI_TaxID=11864; [1]
                                           V-ERBB
                               Avian leukosis virus
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                                                                                                                                                                                    QGGAAPQPH----
                                                                                                                                                                                                        N----NPNQNNMAAVGVAAGYM
                                                                                                                                                                                                                             DVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL----TP
                                                                                                                                                                                                                                                                     DG----DLGMGAAKGLQSLTTHDRSPTQRYSEDTVPLPSETDGYVAPLTCSPQPEYVNQP
                                                                                                                                                                                                                                                                                                                                                           RMARDPORFVVIQUEDLG--PASPLDSTFYRSLLEDD---DMGDLVDAEEYLVPQQGFFC
                                                                                                                                                                                                                                                                                                                                                                                                   FGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFS
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                                                                                                                                                                                                                                                   DSSAREVGVGNLR-----
                                                                                                                                                                                                                                                                                                                 PDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP-----RSPLAPSEGAGSDVF
                                                                                                                                                                                                                                                                                                                                     EFARDPGRYLAIPGDKFTRLPA-----YTSQDEKDLIRKLAPTTDGSEAIAKPDDYLQ 1248
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                                                                                                                                                                                                                                                                                               PKAAPGPS----
                                                                                                                                                                                                                                                                                                                                                                                 FGORPHENIPAKDIPDLIEVGLKLEOPEICSLDIYCTLLSCWHLDAAMRPTFKOLTTVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKIRKYT--MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHVNYQYTAIGPYCAASPPRSSKITANLDVNMIFIITGAVLVPTICILCVV--TYICRQK
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                    Retroviridae;
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protein (
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                 Alpharetrovirus
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                                                                                                                                                                                                                                                                                           DEMPKLNRYCKDPSNKNSSTGDDER
                                                   erbB
                                                                                                                                                                                                      DLIGVPVSVDNPEYLLNAQTL
                                                   (EC 2.7.1.112)
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Best Local (
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BINDING
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SEQUENCE
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DOMAIN 1:
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PRINTS; PRO0109; TYRKINASE.

PRODOM; PD000001; Euk pkinase; 1.

SMART; SN00219; TYRKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

Glycoprotein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A00643; TVCHLV.
PIR; B00643; TVFVLV.
HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M10066; AAA48763.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 41:719-726(1985).
-!- CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nilsen T.W., Maroney P.A., Goodwin R.G., Crittenden L.B., Raines M.A., Kung H.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino-truncated EGF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=85228222; PubMed=2988784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYTOSINE PHOSPHATE.

MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CE IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VI AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                               MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                                                                                                                                                                                    RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                         NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                                                                                                                                                                                                                  APNOAHLRILKETEFKKVKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANK
                                                                                                                                     ETLDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW
                                                                                                                                                                                                                                                                                                                                                                                                                        CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E705E33A0BE01FCC CRC61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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; ATP-binding; (
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RESULT 13
ERBB_AVIER
                                                                                                                                                                                         SEQUENCE OF 1-152 FROM N.A.

MEDLINE=84223957; PubMed=6338658;

A Debuire B, Henry C., Benaissa M., Biserte G., Claverie
Saule S., Martin P., Stehelin D.;

"Sequencing the erbA gene of avian erythroblastosis vii
new type of oncogene.";

Science 224:1456-1459(1984).

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP
tyrosine phosphate.

-i- DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBRO
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00535;
21-JUL-1986
21-JUL-1986
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                         gene
Cell
[2]
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto T., Nishida T., Miyajima N., Kaw
"The erbB gene of avian erythroblastosis
gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84026539; PubMed=6313229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; Retroid viruses; NCBI_TaxID=79685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian erythroblastosis virus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERBB
                                                                                                                             IN CHICKENS: V-ERBB IS A TRUNCATED AND MUTATED VERSION RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cus (strain ES4).
Retroviridae; Avian
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sis virus is a
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Best Local
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NP BIND

BINDING

ACT SITE

CONFLICT

CONFLICT
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PROSITE; PS001107; PROTEIN KINASE ATP;
PROSITE; PS001109; PROTEIN KINASE TYR;
PROSITE; PS50011; PROTEIN KINASE DOM;
Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02006; AAA42394.1;
EMBL; K01216; AAA42400.1;
PIR; A00644; TVYUH.
HSSP; P11362; 1FGK.
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ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
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InterPro; IPR001245; Tyr_
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NLYYWDODPPERGAPPSTFKGTPTAENPEY 1248
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                               -- VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-
                                                                                         FLEESIDDGFL-----PAPEYVNQ--LMPKKPSTAM----
                                                                                                                          LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1177
                                                                                                                                                                                                                                           YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHRHRSSSTRSGGGDLTLGLE 1064
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                                                                                                                                                                                                                                                                                                      ICTIDYYMIMVKCMMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
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                                                              NGVVKDVFAF--
                                                                                                                                                                                                                                                                                    ICTIDVYMIMVXCWMIDADSRPKFRELIAEFSKMARDPPRYLVIQGDERMHLPSPTDSKF
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                                                                                                                                                                                       PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1119
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY)

BY SIMILARITY

BY SIMILARITY

R -> W (IN REF. 2).

S -> F (IN REF. 2).

I -> V (IN REF. 2).
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Pred. No. 9.6e-84;
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                                                     -----GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD
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Matches 341;
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Best Local
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BINDING
ACT SITE
VARIANT
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01-JUL-1989
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVIEU
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERBB
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not recoved. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenotype to ts167 avian erythroblastosis virus-transformed cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Be
"A single amino acid substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11273;
                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=103898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian erythroblastosis virus (strain ts167)
Viruses; Retroid viruses; Retroviridae; Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A25231; TVFVEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M13179; AAA42401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                  766
                                             118
                                                                                                                              647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell. Biol. 6:1751-1759(1986).
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                                                                                                                                                                                                                             Similarity
                                                          MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
                                                                                                                                                    CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                                                                                                                               CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQ
                EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
                                          APNOAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELREATSPKANK
                                                                                                NGSKTPSTAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE
540
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(Rel. 11, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                      Phosphorylation.
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165
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270
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                                                                                                                                                                                                             69;
                                                                                                                                                                                                            Score 1630; D
Pred. No. 6.5e
69; Mismatches
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ATP (BY SIMILAR)
ATP (BY SIMILAR)
BY SIMILARITY.
H -> D (IN THER)
                                                                                                                                                                                                                                                                   -> D (IN THERMOLABILE V-ERBB).
5B53297AA068B65D CRC64;
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on in
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                                                                                                                                                                                                                          DB 1;
.5e-80;
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                                                                   765
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RESULT 15
EGFR CHICK
ID EGFR CHICK
AC P1387;
AC P1390 (
DT 01-JAN-1990 (
DT 15-JUN-2002 (
DE Epidermal gro
(Fragment).
GN Gallus gallus
OC (Fragment).
GN Gallus Gallus
Archosauria;
AC Gallus
ARCHITTAXID=90
RN [1]
AND ALSO
CC ATALYTIC
CC -!- GUNGCELLAN
CC -!- GUNGCELLAN
CC -!- SUBCELLUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler M., Ullrich A., Vennstrom B., Schlessinger J., Givol D., "Chicken epidermal growth factor (EGF) receptor: CDNA cloning, expression in mouse cells, and differential binding of EGF and transforming growth factor alpha.";

Mol. Cell. Biol. 8:1970-1978(1988).

-i- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL CAND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine = ADP + protein
This SWISS-PROT entry is copyright. It is produced through a content of the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
``~~^~~**'a: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=88261272; PubMed=3260329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Epidermal growth factor receptor precu
                                                                                                                                                                                                                              synthesis, a -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                     tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor complex,
induction of the tyrosine kinase activity, stimulation of
synthesis, and cell proliferation.
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TO THE EGF RE
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                                                                                                                                                           collaboration
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                                                                                                                                 outstation
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Tyrosine-protein kinase; ATP-binding; Phosphorylation.
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Pfam; PF00757; Furin-like; 1.
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                                                                                                PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDQYIKANSKFI
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                AVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
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                                                           VKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---NGSKTPSIAA
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Search completed: July 22, 2003, 08:44:44
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

DR HSSP; P11362; 1FGK. DR InterPro; IPR002040; EGFR L domain. DR InterPro; IPR0001719; Euk pkinase. DR InterPro; IPR002174; FurIn-like. DR InterPro; IPR002174; FurIn-like. DR InterPro; IPR001245; Tyr pkinase. DR InterPro; IPR001245; Tyr pkinase. DR InterPro; IPR001245; Tyr pkinase. DR Pfam; PP00757; FurIn-like; 1. DR Pfam; PP009059; pkinase; 1. DR Pfam; PP01030; Recep L domain; 2. Pfam; PP01030; Recep L domain; 2. DR Pfam; PP000001; Euk pkinase; 1. DR Pfam; PP00001; Evk pkinase; 1. DR Pfam; PM00261; FU; 3. DR PROSITE; PM00219; TYFKC; 1. DR PROSITE; PS000107; PROTEIN KINASE DOM; 1. DR PROSITE; PS000107; PROTEIN KINASE TYR; 1. DR PROSITE; PS000109; PROTEIN KINASE TYR; 1. DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.	SULT 1 018735 018735 018735 019735 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence upd. 01-JUN-2002 (TrEMBLrel. 21, Last annotation uperba-2. Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertel Mammalia; Eutheria; Carnivora; Fissipedia; Cannon NCBI_TaxID=9615; 11] SEQUENCE FROM N.A. Yokota H.; "CDNA cloning of erbB-2 from canine mammary ground control of the EMBL/GenBank/DDBJ SUBMitted (CCT-1997) to the EMBL/GenBank/DDBJ EMBL; AB008451; BAA23127.1;
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                                                                            HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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                                                                                                                                                                                                                                                                                                                                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPLEGGIPAPGAAQGGLRELQLRSLTEILKGGVLIQRSPQLCHQDTILWKDVFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKF
                      IDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                            YVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNMCVQIAKGMSYLEDVR
                                                                                                                    YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNMCMQIAKGMSYLEDVR
                                                                                                                                                                                                                                                   VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                         PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
                                                                                                                                                                                                                                                                                                                                        AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLIDTNRFSACPPCSPACKDAHCWGASSGDCQSLTRTVCAGGCARCKGPQPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                IGITELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
              IDSECRPRERELVAEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                          ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                                                                                                                                                                                          VEECRVLQGLPREYVKDRYCLPCHSECQPQNGSVTCFGSEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                                                                                                                                                        {	t AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTSCP}
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ilarity 91.1%;
Conservative '
                                              /GVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
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Pred. No. 0;
42; Mismatches
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                                        Query Match
Best Local
Matches 64
                                                                                  A Guttridge K. Dawson T.L. Earp H.S.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

REMEL; M37394; AAF14008.1; -.

RHSSP; P11362; 1FGK.

RINterPro; IPR000494; EGFR_L_domain.

InterPro; IPR000719; Euk_pkinase.

RINterPro; IPR0012174; Furin-like.

RINterPro; IPR0012174; Furin-like.

RINterPro; IPR0012745; Tyr_pkinase.

Pfam; PF00757; Purin-like; 1.

Pfam; PF00757; Purin-like; 1.

Pfam; PF00059; pkinase; 1.

RPfam; PF00019; Recep L_domain; 2.

PRINTS; PR00109; TYRKINASE.

PRINTS; PR00109; TYRKINASE.

RPROSITE; PS00101; Euk_pkinase; 1.

RPROSITE; SM00261; FU 3.

RPROSITE; PS00107; PROTEIN KINASE_DOM; 1.

PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

RROSITE; PS00109; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QX70
Q9QX70;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epidermal EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FISHER; TISSUE=LIVER; Petch L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A truncated, secreted form of the epidermal growth factor receptor encoded by an alternatively spliced transcript in normal rat tissue. Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                                                                       STRAIN=FISHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Earp H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                   Match
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                                         al Similarity
640; Conser
                w
LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQPDVRPQPPSPREGPLPAARPAGATLER-----AKTLSPGKNGVVKDVFAFGGAVENPE
                                                                                                                                                                                                                                                                                                                                                                    FROM
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                                        Conservative
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A
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    Created)
    Last sequence update)
    Last annotation update)
    receptor.

                                        166;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                       Score 3165; DI
Pred. No. 6.4e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blasband
                                                   DB 11;
.4e-230;
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                                        355;
                                                                                                                                                                                                                                                                                                                                                                                             databases
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                                        Indels
                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                        kinase
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                                        118;
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                                       Gaps
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APGRDLHYON - - PHSNAVS

-DP----

PERGAPPS

1235 1133

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VKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDM
                                                                                          GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                                                                                                                                                                                         HRIYTHQSDVMSYGVTVMELMTFGSKPYDGIPAGEISSILEKGERLPQPPICTIDVYMIM
                                                                                                                                                                                                                                RRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIM
                                                                                                                                                                                                                                                                                                LEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIL 895
                                                                                                                                                                                                                                                                                                                                            GVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVVGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPD 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSSLSANSN----SSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTFL----
                                     LAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLT
                                                                           EDVVDADEYLIPQQGFF
                                                                                                                                         VKCWMIDADSRPKFRELILEFSKWARDPQRYLVIQGDERMHLPSPTDSNFYRALMEEEDM
                                                                                                                                                                                                                                                                          LEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKMMALESIL
                                                                                                                                                                                                                                                                                                                                                                                                               GIVGGLLFIVV-VALGIGLFMRRRQLVRKRTLRRLLQERELVEPLTPSGEAPNQAHLRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTCPSGIMGENNTL-VWKFADANNVCHLCHANCTYGCAGPGLKGC--QQPEGPKIPSIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP-LTSIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECVDKCNILEGEPREFVENSECIOCHPECLPOTWNITCTGRGPDNCIKCAHYVDGPHCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWTDLHAFENLEIIRGRTKQHGQFSLAVVGLNITSLGLRSLKEISDGDVIISGNRNLCYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATNIKHFKYCTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCPRNYVVTDHGSCVRACGPDYYEV-EEDGVSKCKKCDGPCRKVCNGIGIGEFKDTLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQCAAGCTGPRESDCLVCHRFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNMSMDVQRHLTGCPKCDPSCPNGSCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GITELNRSR---ACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKFI
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                                                        InterPro; IPR000345; CytC heme bind.
InterPro; IPR000494; EGFR_L domain.
InterPro; IPR000194; Euk pkinase.
InterPro; IPR0002174; FurIn-like.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase; 1.
Pfam; PF01030; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOm; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 5.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                       EMBL; AF275364; AAG280:
EMBL; AF275365; AAG280:
EMBL; AF275367; AAG243!
HSSP; P11362; 1FGK.
MGD; MGI:95294; Egfr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EP98;
Q9EP98;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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EGFR.
Mus musculus
PROSITE; PS00190; CYTOCHROME C; UNKNOW PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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Schehl C., Pearsall R.S., Green P.J., Yee D.
Balasubramaniam S., Crossley T.O., Magnuson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRALN=C3H/101, 129/SVJ AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balagubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse alternative Egfr transcripts
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STRAIN=C3H/101, 129/SVJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative genomic sequence analysis
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AF275364; AAG28045.1;
AF275365; AAG28045.1;
AF275367; AAG24386.1;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
rowth factor receptor isoform 1.
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K.E., Danielsen., Lampland A.L., James C.D.,

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1210 AA; 134840 MW; 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GICLTSTVQLITQLMPYGCLLDYVREHKDNIGSQYLLNWCVQIAKGMYYLEDRRLVHRDL
                                                                                                                                     GICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDL
                                                                                                                                                                           GSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLL
                                                                                                                                                                                                                     GVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVL
                                                                                                                                                                                                                                                  NPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVL
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PRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLV
                                                                         AARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVW
                                                                                                                                                              GSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLL
                                                                                                                                                                                                                                                                                             EGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGIMGE
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                                                                                                                                                                                                        -VALGIGLEMRRRHIVRKRTLRRLLQERELVEPLTPSGEAPNOAHLRILKETEFKKIKVL
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Pred. No. 1.7e-
70; Mismatches
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1.7e-227;
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Prodom; PD000001; Euk pkinase; 1.

SMART; SM00251; FU; 3.

SMART; SM00219; TYFKC; 1.

SMART; PS00190; CYTOCHROME C; UNKNOWN PROSITE; PS001343; GRAM POS ANCHORING; UN PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00111; PROTEIN KINASE DOM; 2.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Kinase; Transferase; Tyrosi
                                                                                                                        InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000494; EGFR_L domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0012174; Furin-like.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
Pfam; PF000757; Furin-like; 1.
Pfam; PF01030; Recep_L domain; 2.
PRINTS; PR00100; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
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MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C., G
Altschmied J., Schartl M.;
"Activation of the Xmrk proto-encogene of Xi
overexpression and mutational alterations.";
Oncogene 16:1681-1690(1998).
[2]
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                                                                                                                                                                                                                                                                                                   Submitted (JUL-2000) to the EMBL; U53471; AAD10500.2; -- HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Eukaryota; Metazoa; Cl
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   Tyrosine-protein
                                                                 UNKNOWN
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                    IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD
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IILKCWMIDPSSRPRFRELVGEFSQMARDPSRYLVIQG---NLPSPSDRRLFSRLLSSDD
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Query Match
Best Local Similarity
Matches 535; Conserv
                                                                                                                                                                              PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; Euk pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYPKC; 1.

PROSITE; P800107; PROTEIN KINASE ATP; 1.

PROSITE; PS0011; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00652; TNPR NGFR 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001368; TNFR_c6.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00059; pkinase; 1.
Pfam; PF00130; Recep_L_domain; 1.
Pfam; PF01301; Recep_L_domain; 1.
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Q9W6F6;
01-NOV-1999
01-NOV-1999
01-JUN-2002
                                                                                                                Kinase; Tyrosine-protein kinase.
NON TER 1 1
SEQUENCE 1137 AA; 127927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Distribution of neuregulin-1 (nrg1) a embryonic chick hindbrain."; Mol. Cell. Neurosci. 13:258(1999). EMBL; AF121963; AAD31764.1; HSSP, P11362; IFGK.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Gallus gallus (Chicken).
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
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TISSUB=HINDBRAIN;
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        Conservative
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
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                              39.7%;
  %; Score 2705.5;
%; Pred. No. 3e-1
170; Mismatches
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EMBL; AF056116; AAC34391.1; -..
HSSP; P11362; IFGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0002174; Furin-like.
InterPro; IPR0012174; Furin-like.
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IfterPro; IPR0012174; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
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Pfam; PF000001; Euk pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
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MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
MCBI TaxID=31033;
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                                                                                        HFV-VDGSSCVSVCPPDKMEV--ERGSQRQCELCSGLCPKVCEGTGAE--
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Q9BIH9;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment EGFR.
Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culi
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00129; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L_domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOm; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00219; TYRK; 1.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
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"Cloning, expression and localisation";
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196; Mismatches 395;
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Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=99415951; PubMed=10485918; MEDLINE=99415951; PubMed=10485918; Mederty J.K., Bond C., Jardim A., Adelman "The HER-2/neu receptor tyrosine kinase ge autoinhibitor."; Proc. Natl. Acad. Sci. U.S.A. 96:10869-108
                                                  QBRZXI;

QBRZXI;

O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last seque)
O1-JUN-2002 (TrEMBLrel. 21, Last annot.
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogn.
NCBI_TaxID=10090;
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Doherty J.K., Clinton G.M., Adelman J.

Doherty J.K., Clinton G.M., Adelman J.

Submitted (SEP-2000) to the EMBL/GenE

EMBL; AF177761; AAD56009.2; -

InterPro; IPR000494; EGFR L. domain.

InterPro; IPR0012174; Fuxin-Tike.

Pfam; PF00757; Fuxin-like; 1.

Pfam; PF00757; Fuxin-like; 1.

Pfam; PF00030; Recep L. domain; 1.

SMART; SM00261; FU; I.

SEQUENCE 419 AA; 45472 MW; FECIBE
              SEQUENCE FROM N.A. Strausberg R.;
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Homo sapiens (Human)
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EMBL/GenBank/DDBJ
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Pred. No. 1.1e-127;
9; Mismatches 38;
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EMBL; 50372; AAC60725.1; -...
HSSP; P0332; 1A6S.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001428; Retro M.
InterPro; IPR001425; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase.
InterPro; IPR00145; Tyr_pkinase; I.
Pfam; PF02813; Retro M; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; P000001; PROTEIN KINASE ATP; 1.
SNART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE TOM; 1.
PROSITE; PS00109; PROTEIN KINASE TOM; 1.
PROTEIN KINASE TOM; 1.
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01-NOV-1996
01-MAR-2002
Polyprotein.
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MEDLINE-94203659; PubMed-8152791;
Vennstrom B., Raynoscheck C., Jansson L., Doe
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene
evolution of distinct viral genomes carrying
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Q86712;
                                                                                                                                                                                                                                                  different transforming capacities.";
Oncogene 9:1307-1320(1994).
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Hypothetical protein.
SEQUENCE 367 AA; 40163 M
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Matches 358; Conserv
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                                                                   Vennstrom B., Raynoscheck C., Jansson L., Doe Johnsson A., Beug H.; Johnsson A., Beug H.; "Retroviral capture of c-erbB proto-oncogene evolution of distinct viral genomes carrying different transforming capacities."; Oncogene 9:3307-320(1994).
                           EMBL; S69372; AAC60727.1; HSSP; P11362; 1FGK.
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       IPR000719;
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Euk_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                             Alpharetrovirus
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                                                                                                                                                                                      Doederlein G.,
                                                                                                                       mutant
                                                                                                                                           sequences:
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                                                                                                                       v-erbB
                                                                                                                                                                                      Lhotak V.,
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AC Q8WYV
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AC DT 01-MA
DT 01-MA
DT 01-MA
DT 01-JV
DE Hypat
GN P365
GN P365
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Best Local S
Matches 357
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PRODOM; PD000001; EUK_pkinase; 1.

SMART; SM00219; TYRKC; 1.

SMART; SM00219; TYRKC; 1.

PROSITE; PS00107; PROTEIN KINASE_DOM; 1

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1

TYCOSINE-PROCEIN_kINASE_TYR; 1

TYCOSINE-PROCEIN_kINASE_TYR; 1
                                                             QBWYV0, PRELIMINARY; PRT; 412 AA.
QBWYV0; OPENARY: QBWYV0; PRT; 412 AA.
QBWYV0; QBWYV0
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO Pfam; PF00069;
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357; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SRTPLLSSLSATSNNSATNCID-----RNGQGHPVREDSFVQ
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                                                                                                                                                                                                                                                                                                                                        RAKTLSPGKNGVVKDVF-----
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                                                                                                                                                                                                                                                                                              TAMVONOIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL
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Pred. No. 4
Catarrhini;
                   Craniata; Vertebrata; Euteleostomi;
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Hominidae;
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Matches 330
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growth.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ da EMBL; AF318349; AAL55856.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR00719; Buk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00169; YLD_motif.
Pfam; PF00069; pkinase; I.
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064895;

01-NOV-1996 (TrEMBLrel 0

01-NOV-1996 (TREMBLrel 0

01-JUN-2002 (TrEMBLrel 0

01-JUN-2002 (TrEMBLrel 2

Gag, V-erb-A, V-erb-B prote

GAG, V-ERB-A, V-ERB-B
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M.,
Bruskin A. acids from the retroviral
"Six amino acids from the retroviral
transforming potential of the oncoger
                                                                              Avian erythroblastosis virus.
Viruses; Retroviridae;
NCBI_TaxID=11861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 412 AA; 4
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SMART; SM00219; TyrKc; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wan D.F., Gu J.R.;
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                                                                                                                                                                                                                                                      WVWTCQCEPEGQVRRSPDVSSGSREGLTSAGIKRWEGPPTTSRGTCHARN
                                                                                                                                                                                                                                                                                                         GAVENPEYLTPQGGAALSPTLLLPSAQPSTTSITGTRTHQSGGLHPAPSKGHLRQRTQST
                                                                                                                                                                                                                                                                                                                                   GAVENPEYLTPQGGAAPQP----
                                                                                                                                                                                                                                                                                                                                                APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                        EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICT
                                                                                                                                                                                                                                                                                   YYWD-QDPPER-----
                                                                                                                                                                                                                                                                                                                                                                                                             EAPRSPLAPSEGAGSDVFDGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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Lrel. 01, 1
Lrel. 21, 1
B protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1697.5; ; Pred. No. 8.9e. 5; Mismatches
                                                                                                                                            Created)
Last sequ
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       p J.M., McCarley D.J., Schatzman
roviral gene gag greatly enhance
oncogene v-erb-B.";
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            LGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                034397FF3F27D2BC CRC64;
                                                                                                                                            sequence update)
annotation updat
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                                                                                             Avian
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                                                                                                                                           update)
                                                                                                                                                                                                                                                                                 GAPPSTFKGTPTAEN
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                                                                                            type
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Best Local S
Matches 358
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R Pfam; PF00105; zf-C4; 1.

R PRINTS; PR00047; STROHDFINGER.

R PRINTS; PR000047; Euk pkinase; 1.

R ProDom; PD000005; znf-C4steroid; 1.

R ProDom; PD000035; Znf-C4steroid; 1.

R ProDom; P000035; Znf-C4; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00319; Znf-C4; 1.

R SMART; SM00319; Znf-C4; 1.

R PROSITE; PS00013; NUCLEAR RECEPTOR; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001733; Stdhrmn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OHOGENE 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001628; Znf_C4steroid
    867
                                                                                  988
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X52211; CAA36459.1; JOINED
P10828; 2NLL.
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                                                  HRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP
                                                                                                                          AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFV
                                                                                                                                                                 KQLGADEKEYHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIP
                                                                                                                                                                                  RLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIP
                                                                                                                                                                                                                  VEECRVLQGLPRE-YVNAR-HCLP---------
                                                                                                         ASEISSVLEKGERLPQPPICTIDVYMIMVKCWMSGADSRPKFRELIAEFSKWARDPPRYL
                                                                                                                                                                                                                                                                                        IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLL
                                                                                                                                                                                                                                                                                                                                               RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
                                                                                                                                                                                                                                                                                                                                                                                                    NCTHSCVDLDDKGCPAEQRASPLTSIVSAVV-GILLVVVVLGVVFGILIKRRQQKIRKYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                          PONGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPI
                                                                                                                                                                                                                                                                          I PVAIKELREATS PKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLL
                                                                                                                                                                                                                                                                                                                                 RRLLQERELVEPLTPSGEAPNOAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVT
                                                                                                                                                                                                                                                                                                                                                                                      NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I EKCQESYLLAFEHY I NYRKHNI PHFWSKLLMKVADLRMIGAYHASRFLHMKVECPTELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 6.6e
73; Mismatches
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SRTPLLSSLSATSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein
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es 142;
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 --NSATKCIDRNGGH--
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Best Local S
Matches 345
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X MEDLINE=88217326; PubMed=2897102;

X MEDLINE=88217326; PubMed=2897102;

X MEDLINE=88217326; PubMed=2897102;

X MEDLINE=88217326; PubMed=2897102;

A SCOTTING P., Vennstrom B., Jansen M., Graf T., Beug H., Ha "Common site of mutation in the erbB gene of avian erythro virus mutants that are temperature sensitive for transform Virus mutants that are temperature sensitive for transform T. (1997)

X COMMON STATE (1987)

R EMBL; X06943; CAA30024.1;

R EMBL; X06943; CAA30024.1;

R HSSP, P11362; 1FGK.

R HSSP, P11362; 1FR000721; PEUK_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; 1.

R PfAm; PF000001; Euk_pkinase; 1.

R PF0DOm; P000001; Euk_pkinase; 1.

R PF0DOm; P000001; Euk_pkinase; 1.

R PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q85468;
Q85468;
01-NOV-1996
01-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type
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                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                  DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
               KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
                                                      YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                                                                                                                                      GLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQEREL
                                                                                                                                                                                                                                                                                                                                                                              GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
KGERLPOPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKWARDPPRYLVIQGDERWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1645; DB 15;
Pred. No. 1.2e-115;
0; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - LMPKKPSTAMVQNQIYNYISLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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413
                             995
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RC STRAIN-C37BL/G3; TISSUE-LIVER;
RX MEDLINE-C37BL/G3; TISSUE-LIVER;
RX MEDLINE-C37BL/G3; TISSUE-LIVER;
RX MAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,
RA Fleischmann W., Gaasterland T., Carninci P., Magner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
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Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
NCBI TaxID=10090;
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01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
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STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., I
Lampland A.L., Balasubramaniam
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EMBL; AF214513; AAD44149.
EMBL; AF275366; AAG28047.
EMBL; AF275364; AAG28047.
EMBL; AF275365; AAG28047.
EMBL; AK004914; EBAB23688.
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AF275365; AAG28047 1;
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NNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGC
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Pred. No. 2.10
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Search completed: July 22, 2003, 09:00:28 Job time: 53.3575 secs

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Human tyrosine kin
HER2 transgene pla
Human HER2 (ErbB2)
HER-2/neu protein.
Human HER-2/neu on
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ALIGNMENTS

Human heregulin 2 (Her2).

10-AUG-2000 AAY92620;

(first entry)

AAY92620 standard; Protein; 1255 AA

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Domain
                                                                                                                                                                                                  Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope.
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/label= insertion_region
/note= "suitable for foreign epitope insertion'
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/note= "mature polypeptide"
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Steinaa
Gautam A
This is the human heregulin 2 (Her2) sequence. Immunogenic analogues Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign Thelper epitopes were identified (see features table). The method
                                                   Claim
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                                                               Inducing immune responses to weakly immunogenic, peptide antigens for the treatment of breast and
                                                                peptide
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20-OCT-1998;
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is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).

The met CTL (cy) CTL (sy) B-cell first T human p part of PA and The met when th	od compi g cells ot coxic 1 roup dei helper c M, humar all know ncluding od is us pA is h	
?	e 1255 AA;	
Query Match Best Local Matches 124	h 99.0%; Score 6740; DB 21; Length 1255; Similarity 99.0%; Pred. No. 0; 42; Conservative 4; Mismatches 9; Indels 0; Gaps 0;	
•	1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60 	
on on	1 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120	
121	1 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDQYIKANSKF 180 	
181	1 IGITELNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240 : : :	
241	1 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300 	
30	1 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360	
36	1 IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP 420	
4 4 2 2	1 DLSVFQNLQVIRGRILHNGAYSLTLOGIGISWLGLRSLRELGSGLALIHHNTHLCFVHTV 480	
481	1 PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC 540	
541	1 VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC 600	
601	1 PSGVKPDLSYMPIWKFPDBEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG 660 	
5 6 6 6	31 ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL 720 	
72	1 RKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSP 780	

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       Novel synthetic therapeutic compound for inducing immune response and for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory properties
                                                N-PSDB;
                                                                                                                                                                                                                                            Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunetherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                             16-MAR-2000; 2000US-0527487
                                                                                                                                                                                                                                                                                          Human tyrosine kinase-type receptor, HER-2
                                                                                                                               16-MAR-2001; 2001WO-US40328
                                                                                                                                                                                                Region
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Claim 4; Page 63-67;
69pp;
  English
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The invention relates to synthetic therapeutic compounds (antigenic CC peptides) with enhanced binding to major histocompatibility complex (CMHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful for inducing an immune response in a subject and for use in adoptive immunotherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Polynucleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polynucleotides into host cells. The present sequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide (774-782).

Sequence 1255 8

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Conservative

Similarity

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Pred. No. 0; 4; Mismatches

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ILLVVVLGVVPGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGÅMPNQAQMRILKETEL
                            ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                                                  PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
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     Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid -
                                                                                      25-JUN-1999; 99US-0141316.
16-MAR-2000; 2000US-0189844.
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AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                       VEECRVLQGLPREYYNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                                                   Example
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05-OCT-2000;
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                                                                                         ng tumour characterised by overexpression of epidermal growt
receptor, ErbB or cancer in mammal, comprises administering
rbB antibody-maytansinoid conjugate to the mammal
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                                            is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast, ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.
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Query Match Best Local Simi Matches 1242; Sequence Local Similarity A 99.0%; Score 6740; Pred. No. 0; DB 23; Length 1255;

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                             YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                        DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                        ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                                                                                                           ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
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                                                                                                                                                                                                                                                                                                                                          PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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                                                                                                                                                                                                          PSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVVG
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480

420 420 360 360 300 300 240 180 180 120 120 60

240

840

780 780 720 720 660 660 600 600 540 540 480

840

Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAT40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.

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17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
                                                                           Use of HER-2/neu polypeptides - for eliciting an an HER-2/neu associated malignancy, particularly
                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                   Claim
                                                                preventing
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93US-0033644.
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95US-0414417.
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The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGRR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate.cancers, and may be used as an antigen to vaccinate against
                                                                                                                                                                      {\tt HER-2/neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and prostate cancers -
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RESULT 7
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RESULT 8
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                                            The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynuclectide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonuclectides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
  Sequence
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                IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                    UHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRRFT
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IDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA
                                                                                                                                                                     YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
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                                                                                                                Query Match
Best Local Simi
Matches 1240;
                                                                                                                                                                                                                  The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2).
                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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The present invention describes isolated prepared HER2/neu epitopes (I). CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is CC culture in vitro and binds to a complex of an epitope (1), bound to a CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino (CC acids that have 100% identity with a native peptide sequence of HER2/neu; (CC and a second epitope and the peptide is less than 50 contiguous amino (CC acids that have 100% identity with a native peptide sequence of HER2/neu; (CC and immunostimulant activities, and can be used in vaccines. (I), (II) and (II) are useful for inducing cellular immune responses for the CC monitoring or evaluating an immune response to a tumour-associated (CC antigen when incubated with a T lymphocyte sample form a patient and (CC to a seed in vaccines mean that immunosuppressive epitopes that may be present (CC in whole antigens may be avoided. Selected epitopes may be combined to compare to infectious agents or whole protein antigen is eliminated. The vaccine combined to the cotines provides the opportunity to combine epitopes derived from compared to the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope based anti-tumour compared to the exemplification of the present invention.

CC combine problem of tumour-associated molecules addressing the problem of tumour combined to the exemplification of the present invention.
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                                                                                                                                                                                          The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense oligonucleotide which modulates the expression Epidermal Growth Factor receptor, Her2, is useful for treating inflammation or to prevent infection in humans -
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CC The invention relates to an isolated Her-2/Neu polypeptide composition CC effective for eliciting an immune response. The invention is useful for CC eliciting an immune response in a patient, where the patient is human CC leukocyte antigen (HLA)-844 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer. CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine CC and other compositions for the diagnosis, prevention and treatment of CC human malignancies, for stimulating and/or expanding T cells specific for CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a CC human patient, as probe or primer for nucleic acid hybridisation, to CC selectively form duplex molecules with complementary stretches of the CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full CC length gene from a suitable library, and to direct expression of a CC polypeptide in appropriate host cells. The composition is useful in CC prophylactic or therapeutic applications and for the treatment of cancer, CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-CC associated malignancies. The invention is useful in gene therapy. The CC present sequence is human Her-2/neu protein.
             Query Match
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28-SEP-2000;
21-FEB-2001;
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           The present sequence is that of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins and a c-terminal covereins and cancers. The invention provides Her-2/neu fusion pro
                                                                                                                                                                                                                                                                                                                                          Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
ovarian cancers. proteins, nucleic
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                                           phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.
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                                                              Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynuclectide encoding the polypeptide, or antigen presenting cells expressing the polypeptide
                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Her-2/neu; cytostatic; haematological malignanc acute myelogenous leukaemia; AML; chronic myelogenous chronic lymphocytic leukaemia; myeloma; non-Hodgkin's Hodgkin's lymphoma; T cell therapy.
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28-SEP-2000;
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Matches 1240;
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    Query Match
Best Local
                                                                c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568). X in AAR39583 represents the location of a stop codon in AAQ46083.
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antigen - f
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              EEYLVPQQGFFCPDPAPGAGGWVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
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Search completed: July 22, 2003, 08:40:39 Job time: 43.9774 secs

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ALIGNMENTS

A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 812-909 <rex> A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 A;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell. Biol. 7, 2597-2601, 1987 A;Title: Human HER2 (neù) promoter: evidence for multiple mechanisms for transcription A;Reference number: 157622; MUID:87286898; PMID:3039351 A;Recession: 157622 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <tal></tal></rex>	A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;McCession: B44188 A;Molecule type: mRNA A;Residues: 1-517, 'RALL', 522,'S', 524-654,'V', 656-1169,'A', 1171-1255 <cou2> A;Cross-references: GB:M11730; NID:g183986 R;King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985 A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: 159509; MUID:85272597; PMID:2992089 A;Scession: 159509 A;Accession: 159509 A;Scatus: translated from GB/FMBI/DDBI</cou2>	A;Molecule type: DNA A;Residues: 737-1031 <sem> A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 A;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg Science 230, 1132-1139, 1985 Science 230, 1132-1139, 1985 A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chrown, Reference number: A44188; MUID:86070181; PMID:2999974 A;Accession: A44188 A;Molecule type: DNA A;Residues: 740-910 <coul></coul></sem>	A;Recession: A245/1; MUID:86118663; PMID:30035/7 A;Accession: A245/1; AGNID:86118663; PMID:30035/7 A;Accession: A245/1 A;Moclecule type: mRNA A;Residues: 1-1255 <yam> A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 A;Cross-reference mRNA A;Accession: A25491; MUID:86016729; PMID:2995967 A;Accession: A25491</yam>	RESULT 1 A24571 A24571 A24571 A24571 Protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human Protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alernate names: C-erb-B-2 protein precursor; kinase-related transforming protein e: C;Species: Homo sapiens (man) C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 C;Accession: A24571; A25491; A44188; B44188; IS9509; I57622 R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T Nature 319, 230-234, 1986 A.TBile: Similarity of protein encoded by the human C-erb-B-2 gene to epidermal growtl

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F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <EXT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;20-304/Domain: EGF receptor extracellular domain repeat <EE1>
F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F;395-605/Domain: intracellular #status predicted <TMM>
F;654-675/Domain: intracellular #status predicted <INT>
F;664-675/Domain: protein kinase homology <KIND>
F;718-93/Domain: protein kinase homology <KIND
F;718-93/Domain: protein kinase ATP-binding motif
F;668/124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;668/Binding site: Dys #status predicted
F;753/Active site: Lys #status predicted
F;751/Active site: Lys #status predicted
F;1119,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete C;Function:
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                                                                      VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                  PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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1; Mismatches 14;
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A;Title: The new oncogene encodes an epidermal growth factor receptor-relat A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat new oncogene transmembrane domain 2-thiazolyl]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Status: preliminary protein-tyrosine kinase (EC 2.7.1.112) neu precursor C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #t C;Accession: A24562; A61204 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. R; Bargmann, C.I.; Hung, M Nature 319, 226-230, 1986 Weinberg, #text_change receptor-related 11-Jun-1999

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protein

A; Molecule type: DNA A; Rolecule type: DNA A; Rolecule type: DNA A; Residues: 637-663, 'V', 665-702 < MAS> A; Residues: 637-663, 'V', 665-702 < MAS> A; Rote: authors translated the codon GCA for residue 25 as Val C; Genetics: authors translated the codon GCA for residue 25 as Val C; Genetics: neu C; Superfamily: epidermal growth factor receptor; protein kinase h C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1280/Product: protein-tyrosine kinase neu #status predicted homology phosphoprotein; <MAT>

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',723-988/Domain: protein kinase homology <KIN>
',731-739/Region: protein kinase ATP-binding motif
',731-739/Region: protein kinase ATP-binding motif
',71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #statu
',691/Binding site: phosphate (Thr) (covalent) #status predicted
',758/Active site: Lys #status predicted
',882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
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                                                                       SPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLED
     FTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKC
                                                                                                                  ELRKVKVLGSGAFGTVYKGIWI PDGENVKI PVAI KVLRENTS PKANKE I LDEAYVMAGVG
                                                                                                                               ELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVWAGVG
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                                                                                                                                                                           VGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKET
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                                                                                                                                                                                                            RCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATV
                                                                                                                                                                                                                     RCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAV
                                                                                                                                                                                                                                                      ECVEECRVWKGLPREYVSDKRCLPCHPECQPQNSSETCFGSEADQCAACAHYKDSSSCVA
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llarity 86.7%; Pred. No. 4.2e
Conservative 50; Mismatches
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C;Superfamily:
C;Keywords: ATP
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F;726-734/Regio
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726-734/Region:
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                                                       FIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNDEGRYTFGASCVTACP
                                                                                      PVDIDTNRSRACPPCAPACKDNHCWGASPEDCQTLTGTIAPRAVPAARARLPTDCCHEQC
                                                                                                                                  DPLDNVTTATGRTPEGLRELQLRSLTEILKGGVLIRGNPQLCYQDTVLWKDVFRKNNQLA
                                                                                                                                                                                         ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                          MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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PREGTASPPHPSPAFSPAFDNLYYWDONSSEQGPPPSNFEGTPTAENPEYLGLDVPV
               PQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255
                                                            YVNOSEVOPOPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLV
                                                                             YVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLT 1198
                                                                                                                           EGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDFTLPLPPETDGYVAPLACSPQPE 1143
                                                                                                                                             EGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPE 1138
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RESULT 3

148161

148161

C:Brecursor - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C:Accession: I48161

R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki,

R:Nakamura, T.; Oshijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1254 <RES A;Crose-references: GB:D16295; NII C;Genetics: Gene 140, 251-255, 1994
A;Title: Cloning and activation
A;Reference number: I48161; MUID
A;Accession: 148161 Query Match Best Local Similarity epidermal Conservative protein kinase homology <KIN> protein kinase ATP-binding mo growth 86.6%; Score 5876.5; DB 2; 86.5%; Pred. No. 5.8e-244; Live 58; Mismatches 110; cion of the Syrian hamster neu MUID:94193007; PMID:7908275 NID:g493236; factor receptor; from GB/EMBL/DDBJ PIDN:BAA03801.1; motif protein Length proto-oncogene PID: 9747595 ۲. Gaps **Y** . ;

CELHCPALVTYNTDTFESMPNPEGRYTFGASCVTTCP

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240 240 180 180

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RESULT 4
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C;Species: 15-1
C;Date: 15-1
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           Nature 309,
A;Title: Hu
                                                                  pidermal growth factor receptor precursor - human ;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB;Species: Homo sapiens (man) ;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text_change 11-Jun-1999;Pate: 15-Nov-1984 #sequence revision 27-Nov-1982; A43615; A23062; A05281; A23062; A05281; A25072; A3672; A3672; A3672; A3672; A37615; A23062; A05281; A37615; A23062; A3772; A37615; A
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                                  418-425,
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A;Title: ATP-stimulated interaction between A;Reference number: A38023; MUID:84191554; F A;Contents: annotation; receptor activity
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A;Experimental source: epidermoid carcinoma cell link; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.J. Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093
A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss, J.
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A;Reference number: A05281; MUID:84172183; PMID:6324-
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A;Accession: A00641
A;Accession: A00641
A;Accession: A25772
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
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A;Reference number: A25772; MUID:85270438; PMID:2991899
A;Accession: A25772
A;Accession: A25772
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A;Molecule type: mRNA
A;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-2'
',798-799,'TD',802-811,'R',813-942 <XUY>
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF rec
R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma,
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A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplificatic
A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615
                                                                                                              A;Molecule type: protein
A;Residues: 25-30,'S',32-51;454-467 <WEB>
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros,
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucl
A;Reference number: A60143; MUID:85182650; PMII
A;Accession: A60143
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A;Title: Contributory effects of de Novo transcription &
A;Reference number: A38672; MUID:91107677; PMID:1988448
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R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ull
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110
A;Reference number: $30024; MUID:88217333; PMID:3329716
A; Molecule type: protein
A; Residues: 740-744, X', 746-747
R; Mroczkowski, B.; Mosig, G.; Co
Nature 309, 270-273, 1984
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A; Residues: 1-29 < HA2>
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A; Residues: 713-964 <LIN>
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right, D.A.; Carpenter,
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nington, D.; Ullrich, A.; Wat
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A;Cross-references: GDB:120610; OMIM:131550
A;Cross-references: GDB:120610; OMIM:131550
A;Map position: 7p12 3-7p12 1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Kupwrotae: ATP, autophosphorylation; duplication; glycoprotein; phosphoprotein;
F;1-24/Domain: signal sequence #status predicted <SIG-
F;25-1210/Product: EGF receptor #status predicted <AMAT-
F;25-644/Domain: extracellular #status predicted <EXT-
F;75-300/Domain: EGF receptor extracellular domain repeat <EE1-
F;390-600/Domain: EGF receptor extracellular domain repeat <EE2-
F;664-160/Domain: transmembrane #status predicted <TMM-
F;669-1210/Domain: intracellular #status predicted <INT-
F;710-975/Domain: protein kinase homology <KIN-
F;711-726/Region: protein kinase ATP-binding motif
F:718-726/Region: Cartad-rit madiared internalization eigen
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A;Title: Functional independence of the epidermal growth A;Reference number: A3331; MUID:9000323; PMID:2790960 A;Contents: annotation; internalization signal C;Comment: Binding of EGF to the receptor leads to intern C;Genetics:
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LSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG---ILLV : : : | | : | | | | | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                             NPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVL
                                                                                                      EGEPREFVENSECTQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGE
                                                                                                                                                                            QGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPD
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                                                                                                                                                                                                                                                                                                                                                                                     LEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPQYIKANSKFIGITEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR
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Pred. No. 2.5e-124;
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                         NPEYL
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                                                                                                                                                                            DVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPEYVN
                                                                                                                                                                                                                                          LVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGS
                                                                                                                                                                                                                                                                                     CRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEY
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                                                                                                      Q-SVPKRPAGSVQNPVYHNQPLNP-----
                                                                                                                                QPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYL-TPQ
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                                                                          GGAAPQPHPPPAFSPAFDNLYYWDQ------DP-----PERGAPPSTFKGTPTAE
                                                                                                                                                                                                                                                                    SRPKFRELIIEFSKMARDPORYLVIOGDERMHLPSPTDSNFYRALMDEEDMDDVVDADEY
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                         1249
                                                 PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGS-TAE
                                                                                                     -APSRDPHYQD--PHSTAVGNPEYLNTVQ
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A;Molecule type: mRNA A;Residues: 1-714 <AVI> A;Cross-references: GB:X59698 R;Eisinger, D.P.; Serrero, G. submitted to the EMBL Data Library, epidermal growth factor receptor precursor - mouse ()Species: Mus musculus (house mouse) ()Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 18-Jun-1999 C;Accession: A53183; A43818; \$\overline{S}24942; A28941; \$\overline{S}45325; \$\overline{I49643}\$ R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jen Genes Dev. 8, 39-413, 1994

A;Title: The mouse waved-2 phenotype results from a point mutation in the E(A;Reference number: A53183; MUID:94170986; PMID:8125255 A;Cross-references: GB:U03425
R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givoncogene 6, 673-676, 1991
A;Title: Comparison of EGF receptor sequences as a guide A;Reference number: A43818; MUID:91232866; PMID:2030916
A;Accession: A43818 RESULT A53183 A;Reference number: S24942 A;Accession: S24942 A; Molecule type: mRNA A; Residues: 1-1210 < LUE> A; Accession: A53183 Schlessinger, J.; Givol, June ö D.; Morse, the H.S.; Jenkins, ligand Œ EGF binding

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
C;Genetics:
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
C;Genetics:
A;Gene: EGFR
C;Superfamily: epidermal growth factor receptor; kinase-related transforming protein; phoses
C;Roywords: ATP; growth factor receptor; kinase-related transforming protein; phoses
F;1-24/Domain: signal sequence #status predicted <TMM>
F;1-24/Domain: protein kinase homology <KIN>
F;720-728/Region: protein kinase homology <KIN>
F;720-728/Region: protein kinase homology <KIN>
F;700-728/Region: protein kinase ATP-binding motif
F;689,055/Binding site: phosphate (Ser) (covalent) #status experimental
F;093/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: phosphate (Tyr) (covalent) #status experimental
F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental
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A;Residues: 969-971, 'K',973-1115,'D' <EIS>
A;Cross-references: EMBL:Z12608
R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and seri
A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epide
A;Reference number: S45325
A;Status: preliminary
a.Molecule type: DNA
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A; Residues: 1-971, Kr., 973-1210 < VER>
A; Residues: 1-971, Kr., 973-1210 < VER>
A; Cross-references: EMBL: X78987; NID: g488830; PIDN: CAA55587.1;
A; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A; Title: Expression of the epidery as a procession of the epidery as a
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                             FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS 423
                                                                                                                                                                     LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE
                                                                                                                                                                                                                                                              ITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
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  EKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDLH
                                                                                                                                                                                                                              CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
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                                                                                           epidermal growth factor receptor precursor - chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) e: C;Species: Gallus gallus (chicken) C;Date: 28-Peb-1986 #sequence revision 05-May-1995 #10;Accession: A27720; A00643
              R;Lax, I.; Johnson, A.; Howk, R.; S.
Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth f.
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A27720;

growth factor (EGF) receptor: MUID:88261272; PMID:3260329

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Sap, J.; Bellot, F.; Winkler, M.; Ullrich,

05-May-1995 #text_change

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A;Accessión: A27720

A;Molecule type: mRNA
A;Residues: 1-1223 <LAX>
A;Cross-references: GB.M20386
R;Cross-references: GB.M20386
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, Cell 41, 719-726, 1985
A;Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing and particular type: mRNA
A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Accession: A00643
A;Molecule type: mRNA
A;Residues: 585-1223 <NIL>
A;Cross-references: GB:M10066
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F;130/Domain: signal sequence #status predicted <SIG>
F;130/Domain: signal sequence #status predicted <AMT>
F;31-1223/Product: epidermal growth factor receptor #status predicted <AMT>
F;31-654/Domain: Exprescription for extracellular domain repeat <EBI>
F;31-654/Domain: EGF receptor extracellular domain repeat <EBI>
F;81-307/Domain: EGF receptor extracellular domain repeat <EE2>
F;655-677/Domain: transmembrane #status predicted <TMM>
F;658-677/Domain: intracellular #status predicted <TMM>
F;678-1223/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #sfatus predicted
F;132,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;54/Active site: Lys #status predicted
F;54/Active site: Lys #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
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CVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAHYKDPPFC
                                                                 MWRSLFATQSQKTKIIQNRNKNDCTADRHVCDPLCSDVGCWGPGPFHCFSCRFFSRQKE
                                                                                                                                   VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE
                                                                                                                                                                                                        TDLYAFENLEI IRGRTKOHGOYSLAVVNLKIQSLGLRSLKEISDGDIAIMKNKNLCYADT
                                                                                                                                                                                                                                                                                                                                               NIDSFKNCTKINGDVSILPVAFLGDAFTKTLPLDPKKLDVFRTVKBISGFLLIQAWPDNA
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RESULT 7
A47253
epidermal growth factor receptor, HER4 - human
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A47253
R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, G.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A;Title: Ligand-specific activation of HER4/p180erbB4, a fourth member of t.
A;Reference number: A47253; MUID:93189574; PMID:8383326
A;Accession: A47253
A;Accession: A47253
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                                                                                                                                                                                                                                           LDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP 1214
                                                                                                                                                                                                                                                                                                                                                                                  L----PAPEYVNQ--LMPKKPS----
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J.M.; Carlton, G.W.; Foy, fourth member of the

epiderma .

A;Molecule type: nucleic acid
A;Residues: 1-1308 <PHO>
A;Residues: 1-1308 <PHO>
A;Residues: 1-1308 <PHO>
A;Residues: Residues: GB:L07868; NID:g337359; PIDN:AAB59446.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinas C;Keywords: ATP; growth factor receptor
F;716-981/Domain: protein kinase homology <KIN>
F;724-732/Region: protein kinase ATP-binding motif kinase homology PID:g337360

724-732/Region: protein kinase ATP-binding motif

L 1008		¥	5
	VYMVMVKCMMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLL	040	2
L 1009	BECRPRFRELVSEFSRMARDPQRFVVIQNED-LGPASPLDSTF	, 951	ર્ક
D 948	ECIHYRKFTHQS	889	뮍
D 950	-gg -gg	891	ð
A 888	KGMMYLEERRLVHRDLAARNVLVKS PNHVKITDFGLARLLEGDEKEYNADGGKMPIKMMA	829	밁
A 890	MSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVP1	831	Ş
A 828	ALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIA	769	В
A 830	VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNV	771	ð
E 76		709	문
E 770	ILD	711	ð
 A 708	IAAGVIGGLFILVIVGLTFAVYVRRKSIK-KKRALRRFL-ETELVEPLTPSGTAPNQA	653	밁
A 710	TSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQA	652	ર્ક
L 652		596	망
L 651	GVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPL	603	ş
D 595	CNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNCVEKCPD	536	밁
S 602	lpreyvnarhclpchpecop-QngsvTcfgpeadocvacahykd	544	á
S 535	TLFSTINGRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIES	476	В
E 543	RNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQI	484	Ś
T 475	VFSNLVTIGGRVLYSGLSLLILKQQGITSLQFQSLKEISAGNIYITDNSNLCYYHTINWT	416	Д
D 483	VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD	424	Ś
S 415	FINCTKINGNLIFLVTGIHGDPYNAIEAIDPEKLNVPRTVREITGFLNIQSWPPNMTDFS	356	멍
S 423	AGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWI	364	S
: X 355	V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTVDSSNIDK	298	밁
E 363	STD	304	á
: F 297	CSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNF	238	뮍
Y 303	臣	244	ð
G 237	SGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYG	179	Дb
G 243	KGSRCWGESSEDCQSLTRTVCAGGC	185	Ş
: V 178	NFGLQELGLKNLTEILNGGVYVDQNKFLCYADTIHWQDIVRNPWPSNLTLV	128	밁
I 184	NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI	125	Ş
G 127	IEHNRDLSFLRSVREVTGYVLVALNQFRYLFLENLRIIRGTKLYEDRYALAIFLNYRKDG	68	멍
N 124	LPTNASLSFLODIOEVOGYVLIAHNOVROVPLORLRIVRGTQLFEDNYALAVLDNGDDLN	65	ક
	WWWSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEITS	8	밁
Y 64	STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE	9	ş
28;	42.9%; Score 2909.5; DB 2; Length 1308; Similarity 44.9%; Pred. No. 3.6e-117; 5; Conservative 182; Mismatches 386; Indels 173; Gaps	Query Match Best Local S Matches 605	

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120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQL 179

Дb	8	₽	Ş		ş	망	δ	В	8	Вb
1260 QEYSTKYFYKQNGRIRÞIVAENÞEYL 1285	1238 KGTPTAENPEYL 1249	1200 DEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHPDYL 1259	1213FSPAFDNLYYWDQDPPERGAPPSTF 1237	1168 ENPFVSRR	1154 EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPA- 1212	1117 PHYQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE	1101 LPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPBYVNQPDVRPQPPSPR 1153	1057 TPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCNGTLRKPVA 1116	1070 APRS	1009 DEEDLEDMMDAEEYLVP-QAFNIPPPIYTSRARIDSNRSEIGHSPPPAY 1056
		Онрраг 13	-PPSTF 12	-PPKAE 11	НРРРА- 12	1167	QPPSPR 11	LRKPVA 11	AKGLQS 1100	SPPPAY 10

A;Gene: mrk
A;Gene: mrk
A;Map position: Y
C;Superfamily: epidermal growth factor receptor; phosphotransferase; transmembrane protein; C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; F;1-25/Domain: signal sequence #status predicted <SIG>F;1-25/Domain: signal sequence #status predicted <SIG>F;26-156/Product: kinase-related transforming protein (Tu) #status predicted <MAT>F;707-972/Domain: protein kinase homology <KIN>F;707-972/Domain: protein kinase ATP-binding motif 밁 Ś В S Query Match Best Local Similarity Matches 567; Conserv 3 60 4 AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 0 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN LEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSN AALLQ--LLLVLSISRCCSTDPDRKVCQGTSNQMTM----LDNHYLKMKKMYSGCNVVLEN Conservative 162; 38.4%; Score 2609; Pred. No. 2. Mismatches DB 1; 2.2e-104; Length 1166; Indels 138; Gaps 62 59 28; .c

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TWILLPHAPERCOCOCCOHGSCWAPEGPGHCOKFTKLLCARGEVERGEREDICCNE SKIGITELKHISDCLACLIFFNISGISCHAPCHAUTYYTTDTESBWAPEGRZYFGASCYTA HCAGGTGFRATDCLACLIFFNISGISCHIFCPALITYYTTDTESBWAPEGRZYFGASCYTA HCAGGTGFRATDCLACREPWIGGTCCDTCPPRKITDTUSHQVDNENIKYTEGAACYKE CPWYLSTDVOSCTLVCPLHNQEVTARDGTGRCESCKSKEPCAVCYGLGMHLAERGRAPDS	·123 YQK-NPSSPDVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP 179
Db 1150 Nukrió 1156 REGUIT 9 REGUIT 1916 (Accession (acn)) Cipacies (4-Oct.1991 Hesquence_revision 11-Jan.1993 ftext_change 17-Nov-2000 (Accession ASS21) 15144 (Accession ASS21) 1614 (Accession ASS22) (Oy 1244 ENPEYLG 1250

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JC4387

epidermal growth factor receptor homolog precursor -:
epidermal growth factor receptor homolog precursor -:
N;Alternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #t.
C;Accession: JC4387
R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.1
Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characteri.
A;Reference number: JC4387; MUID:96096535; PMID:85221:
A;Accession: JC4387
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A;Experimental source: liver
A;Note: The authors translated the codon AAC for residu
C;Comment: This protein is a functional heregulin recep
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C;Genetics:
A;Gene: ErbB3
A;Gene: ErbB3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; tra
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Product: epidermal growth factor homolog #status predicted
F;640-659/Domain: transmembrane #status predicted <TMM>
F;705-970/Domain: protein kinase homology <KIN-
F;713-721/Region: protein kinase ATP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding si
MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
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                                                                                                                                IFKETELRKLKVLGSGVFGTVHKGIWIPEGESIKIPVCIKVIEDKSGRQSFQAVTDHMLA
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A;Molecule type: mRNA
A;Roslecule type: mRNA
A;Residues: 1-698 cNIL>
A;Cross-references: GB:M10066; GB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g21
A;Cross-references: GB:M10066; GB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g21
A;Cross-references: GB:M10066; CB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g21
A;Rote: in Genbank entry CHKERBBF, release 109.0, the source is designated as G
C;Comment: This protein is synthesized as a gag-env-erbB protein.
C;Genetics:
A;Gene: gag-env-erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-s
F;1-6/Product: gag protein (fragment) #status predicted <GAG-
F;7-59/Product: env protein (fragment) #status predicted <GNV-
F;00-698/Product: protein-tyrosine kinase erbB #status predicted <ERB-
F;194-459/Domain: protein kinase homology <KIN-
F;202-210/Region: protein kinase ATP-binding motif
F;229/Active site: Lys #status predicted
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A;Title: c-erbB activation in ALV-induced erythroblastosis: n A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Accession: B00643
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                  DDKGCPAEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETEL
                                                                  GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGP 116
                                                                                                            GPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDL
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  Score 1766.5; DB 1;
Pred. No. 1.3e-68;
0; Mismatches 137;
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RESULT 12
A;Residues: 1-604 <YAM>
A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA42400.1; PID:g209678
R;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Sau
                                                                                Cell 35, 71-78, 1983
A;Title: The erbB gene of avian erythroblastogis virus is
A:Reference number: A00644; MUID:84026539; PMID:6313229
                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain cyspecies: avian erythroblastosis virus (cyspecies: avian erythroblastosis virus C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999 C;Accession: A00644; A38022 C;Accession: A00644; A38022 R;Yamamooto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.
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                                                                                                                                                       T.; Miyajima,
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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyre F;130-395/Domain: protein kinase homology <KIN>F;138-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted A;Molecule type: DNA A;Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 A;Cross-references: GB:KO2006 C;Genetics: Science 224, 1456-1459, 1984 A,Title: Sequencing the erbA gene of A,Reference number: A38022; MUID:8422 A,Accession: A38022 ;Superfamily: ep; ;Keywords: ATP; ie of avian):84223957; erythroblastosis PMID:6328658

virus reveals a new

type

tyrosine-specific

Length

604;

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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus C.Species: avian erythroblastosis virus C.Species: avian erythroblastosis virus C.Date: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997 C.Accession: 335745
R.Vennstroem, B.
submitted to the EMBL Data Library, March 1993
A.Reference number: S35743
A.Reference number: S35743
A.Reference number: S35745
A.Cession: S35745
A.Cession: S35745
A.Cession: S35745
A.Cross-references: EMBL:X12707
C.Seperfamily: epidermal growth factor receptor, protein kinase homology C.Superfamily: epidermal growth factor receptor, protein kinase homology C.Superfamily: epidermal growth factor receptor, protein kinase homology C.Superfamily: protein kinase homology c.Superfamily: protein kinase ATP-binding motif F;135-400/Domain: protein kinase ATP-binding motif F;170/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                           SSPYWIQSGNHQ---
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Pred. No. 5.8e-66;
76; Mismatches 128;
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RESULT 14
S00727
Kinase-related transforming protein (erbB) (BC 2.7.1.-) -
Kinase-related transforming protein (erbB) (BC 2.7.1.-) -
C.Species: avian erythroblastosis virus
C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_C.
C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #sequence_re
                                                                   C;Keywords: ATP; F
F;135-400/Domain:
F;143-151/Region:
                                                                                                                                                                                                        A;Accessium.
A;Molecule type: DNA
A;Residues: 1-545 <SCO>
A;Residues: 1-545 <SCO>
                                                                                                                                                                                                                                                                                           Oncogene Res. 1, 265-278, 1987
A;Title: Common site of mutation in the erbB gene of avian A;Reference number: S00727; MUID:88217326; PMID:2897102
A;Accession: S00727
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                                                                 ;Superfamily: epidermal growth factor receptor;
;Keywords: ATP; phosphotransferase
;135-400/Domain: protein kinase homology <KIN>
;143-151/Region: protein kinase ATP-binding moti
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Best Local Similarity
Matches 345; Conserv
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54.9%;
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Pred. No. 1.3e-63;
70; Mismatches 121;
  Score
Pred.
1640;
No. 2.
                                                                      <KIN>
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A;Cross-references: GB:X52211
C;Genetics:
A;Gene: erbB
C;Superfamily: epidermal growth
C;Keywords: ATP; phosphotransfe
F;130-395/Domain: protein kinas
F;138-146/Region: protein kinas
                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4) (.) Species: avian erythroblastosis virus (c.) Species: avian erythroblastosis virus (c.) Species: avian erythroblastosis virus (c.) Accession: B44776 (c.) Bishop, J.M.; McCarley, D.J.; Schatzman, R.C. (c.) Oncogene 5, 15-24, 1990 (c.) Bishop, J.M.; McCarley, D.J.; Schatzman, R.C. (c.) Artitle: Six amino acids from the retroviral gene gag greatly enhance the transforming A; Reference number: A44776; MUID:90206603; PMID:1969616 (c.) B44776 (c.) B44
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Matches 340
                                                                                                              Superfamily: epidermal growth factor receptor; protein kinase homology; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase; 130-395/Domain: protein kinase homology <KIN>;138-146/Region: protein kinase ATP-binding motif
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6789
1 MELAALCRWGLLL
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     SwissProt_40:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ERB2 HUMAN
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ERB
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               062799 rattus norv
062799 rattus norv
070412 drosophila
070534 avian eryth
11273 avian eryth
11387 gallus gallu
170424 mus musculu
072464 mus musculu
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072466 mus musculu
1714616 homo sapien
1714616 homo sapien
1714617 cavia porce
1725410 lymnaea sten
1714617 cavia porce
1725410 lymnaea tten
174617 mus musculu
174616 homo sapien
174617 cavia porce
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175617 mus musculu
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P00533 homo sapien
Q01279 mus musculu
Q15303 homo sapien
Q62956 rattus norv
P13388 xiphophorus
P21860 homo sapien
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P04412
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P06494 rattus norv
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~	Q91571 xenopus lae	Q91736 xenopus lae	P53356 hydra atten	Q91738 xenopus lae	Q00944 gallus gall	P54762 homo sapien	Q07494 gallus gall	P09759 rattus norv	P29317 homo sapien	P09208 drosophila	٠.

ALIGNMENTS

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-:- CAPALITIC ACTIVITY: AIP + a protein tyrosine = ADP + protein tyrosine phosphate!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL)!- SUBCELLULAR LOCATION: Type I membrane protein.	ALTHOUGHT ACTIVITY VERY ACTIVITY OF A NEUREGULIN RECEPTOR COMPANY OF A NEUREGULIN RECEPTOR COMPANY OF ALTHAU FOR THIS RECEPTOR. NOT ACTIVATED BY EGF. ALTHA AND AMPHIREGULIN.	EDILINE 93.94196; PIDMED = 8099488; hsani A., Low J., Wallace R.B., Wu A.M.; Characterization of a new allele of the human BRBB2 gene becific competition hybridization."; enomics 15:426-429(1993).	SEQUENCE OF 737-1031 FROM N.A. MEDLINE=86016729; PubMed=2995967; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Semba K., Kamata Drotooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma."; Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985). [4] VARIANTS VAL-654 AND VAL-655.	SEQUENCE FROM N.A. MEDLINE=86070181; PubMed=2999974; COUSSENS L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., MCGTath J., Seeburg P.H., Libermann T.A., Schlessinger J., Francke U., Levinson A., Ullrich A.; "Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene."; Science 230:1132-1139(1985).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDIJINE-86118663; PubMed=3003577; Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N., Saito T., Toyoshima K.; "Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor."; Nature 319:230-234(1986).	13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-UIN-2002 (Rel. 41, Last annotation update) 15-UIN-2002 (Rel. 41, Last annotation update) Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112) (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell surface receptor HER2) (MLN 19). ERBB2 OR HER2 OR NGL OR NEU. Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID-9606;	JUT 1 2 HUMAN ERB2 HUMAN STANDARD; PRT; 1255 AA. P04636;

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Pfam; PF00069; pkinase; T.

Pfam; PF000757; Furin-like; 1.

Pfam; PF01030; Recept_domain; 2.

Pfam; PF01030; Recept_domain; 2.

Pfam; PF00757; YLP; 2.

ProDom; PD000001; Buk_pkinase; 1.

R PRODOM; PN00219; TyrKC; 1.

R SMART; SM00261; FU; 3.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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PIR; A25491;
PIR; A24571;
HSSP; P11362
Genew; HGNC:
MIM; 164870;
       SIGNAL
CHAIN
DOMAIN
DISULFID
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LL; M11761; AAA35808

LL; M11761; AAA35808

LL; M11763; AAA35808

LL; M11764; AAA35808

LL; M11765; AAA35808

LL; M12036; AAA35978

AA35978; AA35978

LC; A24571; A24571;

A24571; A24571;

A24571; A24571;

A24571; A24571;
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RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1870; IPR000494; EGFR L domain.
D; IPR000719; Euk pkinase.
D; IPR0002174; Furin-like.
D; IPR001245; Tyr pkinase.
D; IPR004019; YLP morif.
                     3430;
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RECEPTOR PROTEIN-TYROSINE
היישי ACELLULAR (POTENTIAL)
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TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed-3945311;
MEDLINE-86118662; PubMed-3945311;
Accordance of the second secon
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01-JAN-1988 (Rel. 06, Created)

01-JAN-1988 (Rel. 37, Last sequence update)

15-DEC-1998 (Rel. 37, Last sequence update)

15-DUN-2002 (Rel. 41, Last annotation update)

15-DEC-1998 (Rel. 37, Last sequence update)

15-DEC-1998 (Rel. 37, Last sequence update)

16-ECEPTOR (Rel. 37, Last sequence update)

17-ECEPTOR (Rel. 37, Last sequence update)

18-ECEPTOR (Rel. 3
   STRUCTURE BY NMR OF 650-668.
MEDLINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts
                                                                                                                                 "An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncogenic and oncogenic forms of the new protein.";

EMBO J. 11:43-48(1992).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEWREGULIN-RECEPTOR COM-
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF.
ALPHA AND AMPHIREGULIN.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + prote
EMBL; X03362; CAA27059.1; ALT_INIT. PIR; A24562; TVRTNU. HSSP; P11362; 1FGK.
                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: HETERODIMER WITH EACH
THE CONSTITUTIVELY ACTIVATED ON
SUBCELLULAR LOCATION: Type I me
PTM: LIGAND-BINDING INCREASES I
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESIDUES (BY SIMILARITY)
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ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.
ON: Type I membrane protein.
G INCREASES PHOSPHORYLATION ON TYROSINE
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3GF, TGF-
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SMART; SM00261; FU; 3.
SMART; SM00219; TyrKG; 1.
PROSITE; PS00107; PROTEIN KINASE ATE
PROSITE; PS00109; PROTEIN KINASE TYR
PROSITE; PS50011; PBOTTEN
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Pfam; PF01030; Recep L_domain;
Pfam; PF02757; YLP; Z.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
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09; PROTEIN KINASE TYR; 1
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Glycoprotein; Multigene
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ATP-binding; Phosphorylation;
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                                                                                                                                                                                                                                                                       TISSUE-Nerve;

MEDLINE-94193007; PubMed=7908275;

Nakamura T. Ushijima T., Ishizaka Y., Nagao M., Arai M.,

Nakamura T. Ushijima T., Ishizaka Y., Nagao M., Arai M.,

Yamazaki Y., Ishikawa T.;

"Cloning and activation of the Syrian hamster neu proto-oncogene.";

Gene 140:251-255 (1994).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR GP30 IS A

ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A

POPENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-

POPENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-

ALPHA AND AMPHIREGULIN (BY SIMILARITY).

-I- CATALITIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
  This SWIS between the Europ use by modified
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    s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in by non-profit institutions as long as its content is in the content in the content is in the content in the content is not removed. Usage by and for content is not removed.
                                                                                                                                                                       (POTENTIAL).
SUBCELLULAR LOCATION:
PTM: LIGAND-BINDING IN
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SUBUNIT: HETERODIMER WITH EACH
                                                                                                                               SIMILARITY:
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InterPro; IPR001245; Tyr pkinase.

InterPro; IPR004019; YLP motif.

Pfam; PF00069; pkinase; 1.

Pfam; PF00757; YLP; 2.

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R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

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license@isb-sib.ch).
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 SEQUENCE
Reiter J.
Lampland
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Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells."; Nature 309:418-425(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic [4]
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Reiter J.L., Threadgill D.W., Eley G.D., Str
Schehl Sinclair C., Pearsall R.S., Green P.J.
Balasubramaniam S., Crossley T.D., Magnuson
                                                                                                                                                                                                                                                                                                      Tlekis J.V., Gariti J., Niederberger "Expression of a truncated epidermal protein (TEGFR) in ovarian cancer."; Gynecol. Oncol. 65:36-41(1997).
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97256547;
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"A 1.8 kb alternative transcript factor receptor gene encodes a ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ilekis J.V., Stark B.C., Scoccia B.; "Possible role of variant RNA transcripts in the regulation epidermal growth factor receptor expression in human placent Mol. Reprod. Dev. 41:149-156(1995).
                                                                                                                                                                                                                                            TISSUE=Placenta;
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Maihle N.J.;
"Human and mouse alternative extracellular domain of the resubmitted (FEB-1999) to the F
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MEDLINE-85270438; PubMed-2991899;
Ishii S., Xu Y.H., Stratton R.H., Roe

"Characterization and sequence of the
epidermal growth factor receptor gene.
Proc. Natl. Acad. Sci. U.S.A. 82:4920-
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"Contributory effects of de novo transcription of transcript termination in the regulation of hum factor receptor proto-oncogene RNA synthesis.";
J. Biol. Chem. 266:1746-1753(1991).
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MEDLINE=91107677;
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O'Malley B.W.;
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MEDLINE=84245835; PubMed=6330563;
Xu Y.H., Ishii S., Clark A.J.L., Sullivan M.,
Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor cDNA;
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J. Biol. [16]
                                                                                                        Mroczkowski B., Mosig G., Cc "ATP-stimulated interaction and supercoiled DNA.";
Nature 309:270-273(1984).
                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                          MEDLINE=91107677; PubMed=1988448; Haley J.D., Waterfield M.D.; "Contributory effects of de novo
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"The human EGF receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation of an evolutionarily conserved receptor cDNA from human A431 carcinoma ce
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MEDLINE=84191554;
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J.D., Whittle N., Bennett P.,
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85046483; PubMed=6093780;
.A., Gope M.L., Schulz T.
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MEDLINE=98225196; PubMed=9556602;
Abe Y., Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda D.
"Disulfide bond structure of human epidermal growth factor rece
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MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restroy non-profit institutions as long as its content if its and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor. Is suffered in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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TISSUE SPECIFICITY: Expressed in placenta.
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ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170
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SUBCELLULAR LOCATION: Type I membrane
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Q01279;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (E)
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Mammalia; Eutheria;
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MEDLINE=93026370; PubMed=1408137;
MEDLINE=93026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene."; Oncogene 7:1957-1962(1992).
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                                                                                                                                                                                                                                                                                                                                                                                   Luetteke N.C., Phillips H.K., Qiu T.F. Jenkins N.A., Lee D.C.; Jenkins N.A., Lee D.C.; Tenkins waved-2 phenotype results "The mouse waved-2 phenotype results receptor tyrosine kinse.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
STRAIN=B6/C3; TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
MEDLINE=94170986; PubMed=8125255;
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-714 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Genes
                                                                                                                                                                                                      "Comparison of EGF
binding site.";
                                                                                                                                                                                                                                                                    MEDLINE-91232866; PubMed-2030916; Schlessinger J., MEDLINE-91232866; PubMed-2030916; Schlessinger J.,
                                                                                                                                 SEQUENCE OF 969-1117 FROM N.A.
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STRAIN=C3H; Serrero G.; EMBL/GenBank/DDBJ databases. Eisinger D.P., Serrero G.; EMBL/GenBank/DDBJ databases. Strainger D.P., Serrero G.; EMBL/GenBank/DDBJ databases. Submitted (JUN-1992) to the EMBLARIES THE BIOLOGICAL SIGNAL OF SUBMITTED SUBMITT
                                                                                                                                                                            Oncogene 6:673-676(1991).
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                        sequences
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tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein leads to the receptor leads to the MISCELLANBOUS: Binding of EGF to the EGF-receptor completion internalization of the EGF-receptor completion internalization dimerization, the tyrosine kinase activity, stimulation induction of the tyrosine kinase activity, stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation is between the Swiss Institute. There are no restrictions on its the European Bioinformatics Institute. There are no tis in no way use by non-profit institutions as long as its content is commercial than the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; U03425; AAA17899.1;

EMBL; U03425; CAA42219.1;

EMBL; L06864; AAA53029.1;

EMBL; Z12608; CAA78249.1;

EMBL; Z12608; CAA78249.1;

HSSP; P11362; 1FGK.
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MGD; MGI:95294; Egfr. L domain interpro; IPR000719; Euk pkinase. Interpro; IPR002174; Furin-like. Interpro; IPR002174; Tyr pkinase. Interpro; IPR002174; Tyr pkinase. Interpro; IPR001245; Tyr Dkinase. Interpro; IPR001245; Tyr Dkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; EUK_F
SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC;
SMART; SM00219; TYTKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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PROSITE; PS50011;
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C -> W (IN REF. 5).
L -> F (IN REF. 4).
HP -> DR (IN REF. 4).
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J. Biol
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Q15303;
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TISSUE-Fetal brain;
MEDLINE=97476287; PubMed=9334263;
Arrian G.. Paul S., Choi C.J.,
                                                                                                                                                                                                                                               TISSUE=Breast carcinoma;

MEDLINE=93189574; PubMed=8383326;

MEDLINE=93189574; PubMed=8383326;

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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, 
                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS
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                                                 domain isoform of HER4/ErbB4.
differential processing in re
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Carlton G.W.,

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ProDom; PD000001; Euk_Pkina
SMART; SM00261; FU; 4.
SMART; SM00216; TYrKc; 1.
PROSITE; PS00107; PROTEIN
PROSITE; PS00109; PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESS
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED
CERRBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KINNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CERBBELLUM,
PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS,
LUNG, SALLVARY GLAND, AND PANCREAS.

LUNG, SALLVARY GLAND, AND PANCREAS.

LUNG, SALLVARY GLAND, INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUNG, SALIVARY GLANI
PTM: LIGAND-BINDING
RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING EGF-LIKE ROWTH FACTOR, BETACELLULIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate.
SUBUNIT: HOMODIMER OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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P11362;
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); IPR000719; Euk pkinase.
); IPR002174; Furin-like.
); IPR001245; Tyr pkinase.
); IPR004019; YLP motif.
   e splicing.

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01; Euk_pkinase;
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protein; Multigene family; Receptor; Signal;
receptor; Signal;
receptor; Multigene family; Phosphorylation;
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                                                  TLESTINGRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRGRICIES
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RESULT 7
ERB4 RAT
ID ERB4
AC Q629
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                             SEQUENCE FROM
TISSUE=Heart;
              MEDLINE=98221155; PubMed=9553078;
                                                            NCBI_TaxID=10116;
                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                ERB4_RAT
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                                                                                                                                                                                                                                                               QEYSTKYFYKQNGRIRPIVAENPEYL
                                                                                                                                                                                                                                                                                                                 DEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHPDYL 1259
                                                                                                                                                                                                                                                                                                                                                                      ENPFVSRR-----
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    Sawyer D.R.,
                                                                                                                                                                                                STANDARD;
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    Baliga
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                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae
    R.R.,
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    D.J.,
                                                                              Muridae;
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    Han
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; Murinae; Ra
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 InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-iike.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr motif.
Pfam; Pf00757; Furin-iike; 1.
Pfam; PF000757; Furin-iike; 1.
Pfam; PF01030; Recep L_domain; 2.
Pfam; PF01030; Recep L_domain; 2.
Pfam; PF01030; YLP; 2.
PRINTS; PR00109; TYRKINASE.
PRODOm; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 4.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE AT
PROSITE; PS00107; PROTEIN KINASE AT
PROSITE; PS00107; PROTEIN KINASE AT
                                   Transferase;
SIGNAL
CHAIN
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                                                      PS00107; PROTEIN KINASE ATP; 1.
PS50011; PROTEIN KINASE DOM; 1.
PS00109; PROTEIN KINASE TYR; 1.
PS00109; PROTEIN KINASE TYR; 1.
brane; Glycoprotein; Multigene family; Rece
ase: Tyrosine-protein kinase; ATP-binding;
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RECEPTOR PROTE: EXTRACELLULAR POTENTIAL. CYTOPLASMIC (PO

(POTENTIAL

PROTEIN-TYROSINE

KINASE ERBB-4

Receptor; Signal; ing; Phosphorylation.

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                        EMBL; AF041838; AAD08899.1; -. EMBL; U52531; AAC53051.1; -. HSSP; P11362; 1FGK.
                                                                                                                           entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE=Spinal cord; MEDLINE=97184212; PubMed=9030624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in the vertebrate nervous Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marchionni M.A., Kelly R.A.;
"Neuregulins promote survival and growth of cardiac myocytes.
Persistence of ErbB2 and ErbB4 expression in neonatal and adu
ventricular myocytes.";
J. Biol. Chem. 273:10261-10269(1998).
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InterPro; IPR000494; EGFR_L_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTORS (POTENTIAL).

SUBCELULIAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIM CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                       PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION RESIDUES (BY SIMILARITY).
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Matches 60
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603; Conserv
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        HRECAGGCSGFKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCV
                                          ANSKFIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV
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CYS-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY
                                                                                                                                                                          Score 2890; DB 1;
Pred. No. 4.7e-149;
9; Mismatches 395;
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RESULT 8

XMRK_XIPMA

ID XMRK_XIPMA

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InterPro; IPR000494; InterPro; IPR000719; InterPro; IPR002717; InterPro; IPR002290; InterPro; IPR001245; InterPro; IPR001245;
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Schartl M
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MEDLINE-90015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek B., Maueler W.,
Telling A., Robertson S.M., Schartl M.;
"Novel putative receptor tyrosine kinase encoded inducing Tu locus in Xiphophorus.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neotele

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprinodontiformes; Poeciliidae; Xiphophorus.
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16-OCT-2001
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or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Type I membrane protein.
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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Pro; IPR001245; Tyr_pkinase.
PF00069; pkinase; 1.
PF00757; Furin-like; 1.
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LE RECEPTOR WITH PROTEIN-TYROSINE KINASE ACTIVITY.

TY: ATP + a protein tyrosine = ADP + protein
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                             GRCVASCNILLQGEPREAQVDGRCVQCHQECLVQTDSLTCYGPGPANCSKSAHFQDGPQCI
                                                       QECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCV
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                                   MEDLINE=90083234; PubMed=2687875;
Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.
"Isolation and characterization of ERBB3, a third member
ERBBJ/epidermal growth factor receptor family: evidence fc
overexpression in a subset of human mammary tumors.";
Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC (C-erbB3) (Tyrosine kinase-type cell surface receptor
MEDLINE=90311312;
                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                      Homo
                                                                                                                                                                                                    ERBB3 OR HER3.
            EQUENCE FROM
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 PubMed=2164210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Todaro G.J., Shoyab M.,
"Molecular cloning and expression of an addition
"Molecular related gene.";
factor receptor-related gene.";
proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990)
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SECRETED (SHORT FORM)

ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

SHORT SECRETED: FORM, EXIST DUE TO ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT INTERACT INTERACT INTERACT INTERACT INTERACT INTERACT OF THE LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE INTERACT INTERACTION ON TYROSINE INTERACT OF HOMAN MAMMARY TUMORS SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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SUBCELLULAR LOCATION:
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SUBUNIT: HETERODIMER WITH EACH OF
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Y., Sugimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHORT
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ID IS ACTIVATED BY NEUREGULINS: ATP + a protein tyrosine = P
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R InterPro; IPRUULL...

R InterPro; IPRUULL...

R InterPro; IPRUULL...

R Pfam; pF00069; pkinase; 1.

DR Pfam; pF00057; Furin-like; 1.

DR Pfam; pF000757; Furin-like; 1.

DR Pfam; pF000001; Buk pkinase; 1.

R ProDom; pD000001; Buk pkinase; 1.

SMART; SM00261; FU; 3.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00109; PROTEIN KINASE ATP; FALSE NEG.

DR PROSITE; PS00109; PROTEIN KINASE TOM; FALSE_NEG.

DR PROSITE; PS50011; PROTEIN KINASE TOM; Receptor; Signal;

DR PROSITE; PS50011; PROTEIN KINASE TOM; Receptor; Signal;

DR PROSITE; PS50011; PROTEIN KINASE TOM; Phosphorylation; TRANSMEM DOMAIN DOMAIN NP BIND BINDING BINDING ACT_SITE DISULFID DISULFID EMBL; M29366; AAA35790.1; -... EMBL; M34309; AAA35979.1; -... EMBL; S61953; AAB26935.1; -... PIR; A36223; A36223. HSSP; P11362; 1FGK. CHAIN DOMAIN MIM; 190151; -Genew; HGNC:3431; ERBB3. InterPro; IPR000494; EGFR L domais InterPro; IPR000719; Euk pkinase. InterPro; IPR002174; Furin-like. InterPro; IPR001245; Tyr pkinase. 20 20 644 665 709 715 742 186 1342 643 664 1342 1342 723 742 834 194 L_domain. PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY. POTENTIAL.
CYTOPLASMIC (POTENTIAL) EXTRACELLULAR PROTEIN-TYROSINE (POTENTIAL) KINASE ERBB-3

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                            NLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRIYISANROLCYHHSLNWTKV
                                                      NLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQL
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Pred. No. 4.6e
90; Mismatches
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4.6e-120;
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RESULT 10
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ID ERB3
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                                                             Rattus norvegicus ()
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                          Rattue
                       NCBI_TaxID=10116;
  SEQUENCE
                                                                                                                                       ERBB3
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                                                                                                                                                                     002 (Rel. 41, Last sequence update)
002 (Rel. 41, Last annotation update)
protein-tyrosine kinase erbB-3 precursor
  FROM
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                                                               Chordata;
Rodentia;
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Sciurognathi; Muridae;
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[2]
REVISIONS
Hellyer N.
Submitted
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Pfam; PF00757; Furin-like; I.
Pfam; PF01030; Recep L domain;
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 922-1097 FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-SCi
MEDLINE-97184212; PubMed-9030624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=96096535; PubMed=8522190; Hellyer N.J., Kim H.-H., Greaves C.H "Cloning of the rat ErbB3 cDNA and crecombinant protein."; Gene 165:279-284(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Euk_pki
SMART; SM00261; FU; 5.
SMART; SM00219; TYTKC; 1.
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-i- FUNCTION: BINDS AND IS ACTIVATED BY
-i- CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U29339; AAC28498.2; -.
EMBL; U52530; AAC53050.1; -.
HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000494; EGFR L domai
InterPro; IPR000719; Euk pkinase.
InterPro; IPR000174; Furin-ike.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR NET OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PYM: LICAND-BINDING INCREASES PHOSPHORYLATION AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBLAND PROMOTES ITS ASSOCIATION PROMOTES ITS ASSOCIA
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SUBUNIT: HETERODIMER WITH
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V.J., Koland
(DEC-2001)
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PROTEIN KINASE_TYR; 1.
PROTEIN KINASE_DOM; 1.
YCoprotein; Multigene family; Rece
ysoprotein; Kinase; ATP-binding;
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                                                                                                                                KINASE.
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VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDKGCPAEQRASPLTSI
                                          EGVCVTHCNFLQGEPREFVHEAQCFSCHPECLPMEGTS:
                                                                         GQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFC
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                                                       SEQUENCE FROM N.A. (ISOFORMS TYPES I AND II).
MEDLINE=94350209; PubMed=8070664;
Clifford R., Schupbach T.;
"Molecular analysis of the Drosophila EGF receptor homolog
that several genetically defined classes of alleles cluster
subdomains of the receptor protein.";
Genetics 137:531-550(1994).
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13-AUG-1987 (Rel. 05; Created)
15-DEC-1998 (Rel. 37; Last sequence update)
16-OCT-2001 (Rel. 40; Last annotation update)
Epidermal growth factor receptor precursor (EC
(Gurken receptor) (Torpedo protein) (Drosophila
EGFR OR TOP OR C-ERBB OR DER OR CG10079
                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandbulata; Pancrustacea; Hexapoda;

Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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RA Adams M.D., Calniker S.E., Hich RA., Shabburner M., Henderson S.N.,
RA Adams M.D., Calniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Balwin D.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Dodson K., Doup L.E., Downes M., Dugar.Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., 
       STRAIN=Daekwanryeong;
MEDLINE=85137938; Puk
Wadsworth S.C., Vince
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Dev. Biol. 205:129-144(1999).
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Livneh E., Glazer L., Segal D., Schlessing:
"The Drosophila EGF receptor gene homolog:
hormone binding and kinase domains.";
Cell 40:599-607(1985).
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STRAIN=Berkeley;
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                  8; PubMed=2983232;
Vincent W.S. III,
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S.-Y., Katz J..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10731132;
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II, Bilodeau-Wentworth D.; with homology
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SUBCELLULAR LOCATION: ISOFORMS TYPE
SUBCELLULAR LOCATION: ISOFORM TYPE III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), T. TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. II UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE ANTENNA DISK.
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L; AF052754; AAC08536.1; JOINED.
AF052753; AAC08535.1; JOINED.
C; AF052752; AAC08535.1; JOINED.
C; K03054; AAA51462.1; -
C; K03416; AAA51462.1; -
C; K03416; AAA51461.1; -
C; K03418; AAA51461.1; -
C; K03418; AAA51461.1; -
C; K03418; AAA51613.1; -
C; AF109078; AAD2613.2.1; -
C; AF109078; AAD2613.1; JOINED.
AF109084; AAD2613.1; JOINED.
AF109084; AAD2613.1; JOINED.
C; AF109084; AAD2613.1; -
C; AF109084; AAD2613.1; JOINED.
C; AF109089; AAD2613.1; -
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C; AF109089; AAD2613.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND THORACIC AND ABDOMINAL GANGLIA. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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314:178-180(1985).
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n by receptor-tyrosine kinases.";
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Best Local
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00261; FU; 7.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01030; Recep L domain; PRINTS; PR00109; TYRKINASE. ProDom; PD000001; Euk pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000394; EGFR L domai
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0002174; FurIn-like.
InterPro; IPR0012174; Tyr pkinase.
Pfam: PF00069; pkinase; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X78919;
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HSSP; P11362; 1FGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      KICIGTKSRLSVPSNKEHHYRNLRDRYTNCTYVDGNLKLTWLPNENLDLSFLDNIREVTG
                                                                                                                                                                                                                                                                                                                              RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP
                                                                                                                                                                                                                                                                                                                                                                  YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL
LQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCP----
                                            RNPHOALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRV
                                                                                                                             FLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQN
                                                                                                                                                                          PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA
                                                                                                                                                                                                                               LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                                                                                                                                           SCTHG
                                                                                                                                                                                                                                                                              MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPQYIKANSKFIGITELKHSDCLAC
                                                                                                                                                                                                                                                                                                         YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                                                                                                                                                                                                                                                        YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV
                      KEPEQKVWVNENI
                                                                                        LQVIRGRILHNGAY-SLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLF
                                                                                                                  ILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKEITGYLNIEGTHPQFRNLSYFRN
                                                                                                                                                                PODKMDKGGE
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                                                                   LETIHGRQLMESMFAALAIVKSSLYSLEMRNLKQISSGSVVIQHNRDLCYVSNIRWPAIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE ATP; 1.
PROTEIN KINASE TYR; 1.
PROTEIN KINASE DOM; 1.
YCOProtein; Receptor; Pl
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1426
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ATP (BY SIMILARITY)
BY SIMILARITY.
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CYTOPLASMIC
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Signal; Alternative
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                                                  ERBB_ALV STANDARD;
P00534;
21-JUL-1986 (Rel. 01, Cre
15-JUL-1999 (Rel. 38, Las
15-JUN-2002 (Rel. 41, Las
Tyrosine-protein kinase t
           Viruses; Retroid viruses; NCBI_TaxID=11864;
                               Avian leukosis virus.
                                            V-ERBB
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                                                                                                                                                                       QGGAAPQPH----
                                                                                                                                                                                                                               DSSAREVGVGNLR-----
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                                                                                                                                                                                                                                                                       PKAAPGPS-----HRTDCT-----
                                                                                                                                                                                                                                                                                        PDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP-----RSPLAPSEGAGSDVF
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                                                           (Rel. 01, Created)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                           ----NPNQNNMAAVGVAAGYM
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                                                  transforming
                      Retroviridae; Alpharetrovirus
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between
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PIR; B00643; TVFVLV.
                                                                                                                                                                                                                                                           SEQÜENCE
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IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
                                                                                                                                                                                                                                                           634 AA;
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138
165
257
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HSSP; P11362; IFGK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS00109; PROTEIN KINASE TYR; PROSITE; PS50011; PROTEIN KINASE DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=8522822; PubMed=2988784;
Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.N.
Crittenden L.B., Raines M.A., Kung H.-J.;
"C-erbB activation in ALV-induced erythroblastosis:
processing and promoter insertion result in express:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino-truncated EGF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M10066; AAA48763.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYPOSINE PHOSPHALE. PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CE MISCELLANBOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CE IN CHICKS WHICH HAVE BEEN INJECTED WITH THB AVIAN LEUKOSIS VI AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THIS PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                            MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
                                                                                                                                                                                                                                                                                                                             RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                 EILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLLDYIREHKDNIGSQYLLNW
                                                                                                                                  EILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNW
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 1.1
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P00535;
P1-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                           gene
Cell
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=84026539; PubMed=6313229; Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi "The erbB gene of avian erythroblastosis virus is a
                                                                                                                                                                                                                                                                                                                                                                                                                           Avian erythroblastosis virus (strain ES9 Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=79685;
                                                                                                                                                                                                                                                        MEDLINE=84223957; PubMed=6328658; Debuire B., Henry C., Benaissa M., Saule S., Martin P., Stehelin D.;
                                                                                                                                                                                                      "Sequencing the erbA gene of avian erythroblastosis virus new type of oncogene.";
Science 224:1456-1459[1984).
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + F
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-152 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                               SIMILARITY: BELONGS
                                                                                                                                       MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED
                                                                                                                                                                tyrosine phosphate.
DISEASE: THE V-ERBB ONCOGENE
ERYTHROBLASTS IN CULTURE AND
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35:71-78(1983).
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Matches 360
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DOMAIN 13
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BINDING 16
ACT SITE 25
CONFLICT 2
CONFLICT 14
CONFLICT 14
SEQUENCE 604
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EMBL; K01216; AAA424
PIR; A00644; TVYUH.
HSSP; P11362; 1FGK.
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ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TYYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS001109; PROTEIN KINASE DOM;
PROSITE; PS50011); PROTEIN KINASE DOM;
Transferase; Tyrosine-procein kinase;
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InterPro; IPR001245; Tyr_pkinase.
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                            --- VONQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL-----
                                                                                FLEESIDDGFL-----PAPEYVNQ--LMPKKPSTAM--
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AAA42400.1; -.
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S -> F (IN REF. 2).
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Pred. No. 3.3e-85;
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                              -NTNOSPLAKTVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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Viruses; Retroid viruses; Retroviridae; Avian type C
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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3M00219; TyrKc; 1.
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                                                                                                                                 MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                                                             APNQAHLR I LKETEFKKVKVLGFGAFGTVYKGLWI PEGEKVT I PVA I KELREATSPKANK
                                                                                                                                                                                                                                                                                                                                            CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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(Rel. 11, Last sequence update)
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between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                     This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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P13387;
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Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                  Ullrich A., Vennstrom B., Schlessinger J., Givol D.;
"Chicken epidermal growth factor (EGF) receptor: CDNA cloning, expression in mouse cells, and differential binding of EGF and transforming growth factor alpha.";
Mol. Cell. Biol. 8:1970-1978(1988).
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                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88261272; PubMed=3260329;
Lax I., Johnson A., Howk R., Sap J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epidermal
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01-JAN-1990
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                                                                                                                                         tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANDEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complination of the tyrosine kinase activity, stimulation
                                                                                                                                                                                                                                       FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                 SIMILARITY: BELONGS
                                                                                                                                 synthesis, and
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(Rel. 13,
(Rel. 41,
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    Last sequence update)
    Last annotation update)

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TO THE EGF RECEPTOR FAMILY.
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Pfam; PP00757; Furin-like; 1.
Pfam; PP01030; Recep_L_domain; 2.
SMART; SM00261; FU; 4.
PROSITE; PS00107; PROTEIN KINASE AT PROSITE; PS00109; PROTEIN KINASE TY PROSITE; PS00101; PROTEIN KINASE TY PROSITE; PS50011; PROTEIN; RECEPT
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
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182 TLID-TNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPQYIKANS
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09; PROTEIN_KINASE_TYR; F
11; PROTEIN_KINASE_DOM; F
Glycoprotein; Receptor;
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ein; Receptor; Signal; Transferase;
ATP-binding; Phosphorylation.
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112; Mismatches ?
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POTENTIAL.

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                                                  VKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---NGSKTPSIAA
                                                                                                            CVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHFIDGPHC
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GVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTP
                    AVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
                                                                               VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIVS
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Search completed: July 22, 2003, 08:45:06 Job time: 20.2304 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
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11: sp_votent:*
12: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_vrodent:*
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sp_unclassified:*
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sp_phage:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length DB	DВ	ID .	Description
_	6187	91.1	1259	6	018735	Ol8735 canis famil
2	3079	45.4	1209	11	Q9QX70	O9qx70 rattus norv
w	3050	44.9	1210	11	864360	
4	2659	39.2	1165	13	Q9YH40	09vh40 xiphophorus
5	2635.5	38.8	1137	13	Q9W6F6	Q9w6f6 qallus qall
6	2241	33.0	1328	13	P79754	P79754 fugu rubrio
7	1961.5	28.9	1433	տ	Q9BIH9	Q9bih9 anopheles q
8	1766.5	26.0	419	4	Q9UK79	09uk79 homo sapien
9	1739	25.6	367	11	Q8R2X1	O8r2x1 mus musculu
10	1720	25.3	729	15	Q86712	Q86712 avian rous-
11	1718	25.3	567	15	Q86714	Q86714 avian rous-
12	1697.5	25.0	412	4	ONAMBÖ	Q8wyv0 homo sapien
13	1653.5	24.4	962	15	Q64895	Q64895 avian eryth
14	1645	24.2	545	15	Q85468	Q85468 avian eryth
15	1441.5	21.2	655	11	Q9WVF5	09wvf5 mus musculu
16	1425.5	21.0	247		OSERVA	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
586.5	587.5	587.5	590.5	592.5	595	599	602	611	615	622.5	626	626.5	643	648	658.5	683	712.5	754.5	778	806.5	887	906	936.5	971.5	1063	1155	1161.5	1217
8.6	8.7	8.7	8.7	8.7	8.8	8.8	8.9	9.0	9.1	9.2		9.2	9.5	9.5	9.7	10.1	10.5	11.1	11.5	11.9	13.1		13.8	14.3	15.7	17.0	17.1	17.9
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Q9UMQ4	054967	Q07912	Q8UW83	Q9VD94	Q9QVW4	Q99MR2	OMAT60	Q8UW84	Q9BG66	Q8UW86	073798	Q9USA8	093457	Q9BUD7	QBUW85	Q9NJV5	Q9PVZ4	Q99162	Q8SZW1	P11776	Q923V5	Q14256	Q9ESE0	Q9PSH2	Q90836	Q26566	Q23821	8X1X6O
	O54967 mus musculu	Q07912 homo sapien		α.						Q8uw86 paralichthy		Q9u5a8 bombyx mori	O93457 scophthalmu	Q9bud7 homo sapien	Q8uw85 paralichthy	Q9njv5 biomphalari	Q9pvz4 xenopus lae	Q99162 xiphophorus	Q8szwl drosophila	P11776 xiphophorus	Q923v5 rattus norv	homo saj	rattus	Q9psh2 gallus gall	Q90836 gallus gall			Q9y1x8 ephydatia f

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                                                                                                                                                                                                 HQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWM
                                                                                                                                                    YVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVR
                                                                                                                                                                                                                                                                                                                                                  VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                                                                                                                                                                                                                            PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPQYIKANSK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELAALCRWGLLLALLPPGAASTQVCTGTDMXLRLPASPETHLDMLRHLYQGCQVVQGNL
EFYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                 IDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
                                                                                                           LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESIPPRRFT
                                                                                                                                                                                                                                              ILLAVVVGLVLGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETEL
                                                                                                                                                                                                                                                          ILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIIKETEL
                                                                                                                                                                                                                                                                                          PSGVKPDLSFMPIWKFADEEGTCQPCPINCTHSCADLDEKGCPAEQRASPVTSIIAAVVG
                                                                                                                                                                                                                                                                                                    PSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRASPLTSIVSAVVG
                                                                                                                                                                                                                                                                                                                                    VEECRVLQGLPREYVKDRYCLPCHSECQPQNGSVTCFGSEADQCVACAHYKDPPFCVARC
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                                                                          R InterPro; IPR000719; Euk_pkinase.

R InterPro; IPR000714; FurIn-like.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PP00059; Pkinin-like; 1.

R Pfam; PP00059; pkinase; 1.

R Pfam; PP001030; Recept_domain; 2.

R PRINTS; PR00109; TYRKINASE.

R PRONTS; SM00201; Euk_pkinase; 1.

R PROSODOM; PD000001; Euk_pkinase; 1.

R SMART; SM00219; TYRK; 1.

R PROSITE; PS001019; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

SMAPD-binding; Receptor; Transferase; Tyrosine-protein kinase.

SGUENCE 1209 AA; 134891 MW; 96FEE7F6CC1B7773 CRC64;
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Q9QX70;
Q9QX70;
f 01-MAY-2000 (TrEMBLrel. 13,
/T 01-MN-2000 (TrEMBLrel. 21
DT 01-JUN-2002 (TrEMBLrel. 21
Pridermal growth factor re
                                     Query Match
Best Local Similarity
Matches 632; Conserv
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STRAIN=FISHER;
Petch L.A.;
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STRAIN-FISHER; TISSUE-LIVER;
Guttridge K., Dawson T.L., E
Guttridge (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-PISHER; TISSUE-LIVER;
MEDLINE-90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W.,
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Mammalia; Eutheria; Rodentia;
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LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
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                                     Conservative
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                                  Score 3079; D. Pred. No. 1.4e 66; Mismatches
                                                                                                                                                                                                                                                                domain.
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EMBL/GenBank/DDBJ
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1.4e-224;
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                                                                                               SSLSANSN----SSTVACINRNGSCRVKEDAFLQRYSSDPTSVLTEDNIDDTFL--
                     PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--PGYVAPLTCS
                                                                  LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076
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InterPro; IPR000345; CytC heme_bind.
InterPro; IPR000494; EGFR L domain.
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EMBL; AF275365; AAG28045.1; J
EMBL; AF275367; AAG24386.1;
HSSP; P11362; 1FGK.
MGD; MGI:95294; Egfr.
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Q9EP98;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Mammalia; Eutheria; I
NCBI_TaxID=10090;
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balagubramaniam S., Crossley T.O., Magnuson T.R.,
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Mus musculus (Mouse).
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STRAIN=C57BL/6J;
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1210 AA; 134840 MW; 62
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Pred. No. 2.2e-222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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SMART; SM00261; FU; 3.

SMART; SM00219; TYPKC; 1.

SMART; SM00219; TYPKC; 1.

PROSITE; PS00109; CYTOCHROME C; UNKNOWN PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 2.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.
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Q9YH40;
01-MAY-1999
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                           InterPro; IPR000345;
InterPro; IPR000494;
InterPro; IPR000719;
InterPro; IPR002174;
InterPro; IPR001899;
InterPro; IPR001245;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprinodontiformes; Poeciliidae; Xiphophorus.

NCBI_TaxID=8086;
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XMRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock C.,
Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of overexpression and mutational alterations.
Oncogene 16:1681-1690(1998).
                                                                                                                                                                                Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain;
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=RIO PURIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U53471; AAD10500.2; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                               Pfam;
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                                                                                                                                                                                                                                    erPro; IPR000494; EGFR-L domain
erPro; IPR000719; Euk pkinaee.
erPro; IPR002174; Furin-like.
erPro; IPR001899; Gram pos anch
erPro; IPR001245; Tyr pkinase.
m; PF00757; Furin-like; 1.
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 21, Last annotation
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Best Local Similarity
Matches 575; Conserv
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                                                                                                               NYLEERHLVHRDLAARNVLLKNPNHVKITDFGLSKLLTADEKEYQAHGGKVPIKNMALES
                                                                                                                                SYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPENMTSLSVFQNLEIIRGRTTFSRGFSFVVVQVSHLQWLGLSSLKEVSAGNVILKNTFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTH 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LELLEL----LLLLLLSIGRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
IILKCWMIDPSSRPRPRELVGEFSQMARDPSRYLVIQG---NLPSPSDRRLFSRLLSSDD
                  IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDD
                                                                                                                                                                                                                               ILKETEFKKDRVLGSGAFGTVYKGLWNPDGENIRIPVAIKVLREATSPKVNQEVLDEAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRYASTINWRRLFRSEDQSIEYDART-----ENQTCNNECSEDGCWGPGPTMCVSCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVNSTNIGSFSNCTKINGDIILNRNSFEGDPHYKIGPMDPEHLWNLTTVKEITGYLVIMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPKVCDGIGIGSLSNTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKANSKFIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPQY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLENLEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLL 116
                                                                                                                                                                                                                                                                                                                                                POCIPACPHEMLEDEDTL-IWKYADKMEQCOPCHONCTOGCSGPGLSGCRGD-IVSHSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMSNYQK-NPSSP--DVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.2%; Score 2659; DB 13; ilarity 45.2%; Pred. No. 1e-192; Conservative 162; Mismatches 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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     Query Match
Best Local S
Matches 530
                                                                                                                                                                PRINTS; PRO0109; TYRKINASE.

ProDom; PD0000001; Euk Dkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYRKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001368; TNFR c6.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain; 1.
Pfam; PF013757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W6F6
Q9W6F6;
01-NOV-1999
01-NOV-1999
01-JUN-2002
                                                                                                   Kinase; Tyrosine-protein kinase.

NON_TER 1 1

SEQUENCE 1137 AA; 127927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Distribution of neuregulin-1 (nrg1) embryonic chick hindbrain.", Mol. Cell. Neurosci 13:237-258(1999) EMBL; AF121963; AAD31764.1; -... HSSP, P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERBB4.
Gallus gallus (Chicken).
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TISSUE=HINDBRAIN;
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InterPro; IPR000719; Euk_pki
InterPro; IPR002174; Furin-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dixon M., Lumsden A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99263203;
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       530;
                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10328884;
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Neognathae; Galliformes; Phasianidae; Phasiani
                            38.8%;
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Furin-like.
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     167;
  Score 2635.5;
Pred. No. 5.9e
67; Mismatches
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  5.9e-191;
ches 365;
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                                                                                                                                                                     NRNQFVYRDGGYAAEQGV-PMPYRAPGCIIPEAPVAQGATAEIFEDTCCNGTLRKQVATL
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                                                                              PLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----
                                                                                                         AKEDSSTORYSADPTVFIPERVIRGELDEDGYMTPMRDKPKTDYLNPVEENPFVSRRKNG
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Best Local Sim
Matches 515;
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01-MAY-1997
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Pfam; PF00757; Furin-like; 1.

Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep L. domain; 2.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYFKC; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1

PROSITE; PS50011; PROTEIN KINASE DOM; 1

ATP-bindang; Transferase.

SEQUENCE 1328 AA; 148613 MW; A33303;
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MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S.;

"Analysis of 148 kb of genomic DNA
rubripes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 9:251-258(1999).
EMBL; AF056116; AAC34391.1;
HSSP; P11362; IFGK.
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InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                         GTGAE---QRQTVDSSNIDSFINCTKIQGSLHFLVTGILGDDFKNVPPLDAKKLEVFRTV
                    GLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL
                                                                                                                                                        AGCKGPL-
                                                                                                                                                                                           ARCKGPLPQYIKANSKFIGITELKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPN
                                                                                                                                                                                                                              LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-------
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                                                                                                                                                                                                                                                                                                                                                                                           TQIESNWDFSFLKTIREVTGYVLIAMNHFQEIPLGQLRVIRGNSLYERRFALSVFLN---
                                                                                                                                                                                                                                                                                                             ----YPKDG--PSGLNQLGLMNLTEILDGGVQIINNKYLRYGPWVYWRDII-RNNDAPIE
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Last sequence update)
Last annotation update)
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Pred. No. 6.6e-161;
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                                                                                                                                                      DTDCFACRLENDSGACVPQCPQTLIYNKQTFQMBTN
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RESULT
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ID Q9BOOR
AC Q9
DT 01
DT 01
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Q9BIH9;
01-JUN-2001
01-JUN-2001
01-JUN-2002
Putative epi
  Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
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                                                                                                                                                                                                                                                                                                                                                                                            AFRRSSREAELCEDGAQCAGIFRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSYMVMTQLRYD-----FAVSQGGHIGYLPMSPSPVDTIRQLWYQRSRLSSVRTLPDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GLLEADLEEDEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMG---AAKGLQSLPTHDPSPLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKGERLSQPAICTIDVYMVMVKCWMIDENIRPTFKELASDFTRMARDPPRYLVIRMEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEYHADGGKVPIKMMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESFEPLGP-GEKGTKVHARILKPSDLRKIKPLGSGVFGTVSKGFWIPEGETVKIPVAIKT
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Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
idermal growth factor receptor (Fragment)
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RYSEDPTVPLPSETDGYVAPLTCSPQP-EYVNQ------
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                                                                                                                                                                                                                                                                                                       QQRKLSTASSPSSFKTWAADEEDE
                      Tracheata; Hexapoda; Insecta;
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    Culicoidea;
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Pfam; PF00757; Furin-like; 1.

Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep L domain; 2.

PRINTS; PR00109; TYRKINASE.

PRODOM; PD000001; Euk pkinase; 1.

SMART; SM00261; FU; 7.

SMART; SM00261; FU; 7.

SMART; SM00219; TYRK; 1.

SMART; SM00219; TYRK; 1.

SMART; SM00199; CYTOCHROME C; UNKNOWN 4.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
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STRAIN=SUA
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HSSP; P11362; 1FGK.
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"Cloning, expression and localisation "Cloning, expression and localisation epidermal growth factor receptor.";
Submitted (NOV-2000) to the EMBL/GenBa
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[1]
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InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR0001719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                VVGGRQLKENLFASVYIVKTSLKSLELKSLKRVNSGSIVILENSDLCFVEDIDWSEIKKS
                                                                                                                                                                                                                                                                            GKMPQNSE-----CVPCKGVCPKTCPGEGIVH------
                                                                                                                                                                                                                                                                                                                  HNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFL
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to the EMBL/GenBank/DDBJ databases
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6; Mismatches 401;
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InterPro; IPR000494; EGFR L domain InterPro; IPR002174; Furin-like. Pfam; PF01030; Recep L domain; 1. SMART; SM00261; FU; 1
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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
NCBI_TaxID=9606;
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Q8R2X1;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse)
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MEDLINE=99415951; PubMed=10485918;

Doherty J.K., Bond C., Jardim A., Adelma
"The HER-2/neu receptor tyrosine kinase
autoinhibitor.";
  Strausberg R.;
Submitted (APR-2002)
                                             SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=10090;
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Primates; Catarrhini; Hominidae;
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86.3%; Pred. No. 1.2e-125;
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  EMBL/GenBank/DDBJ
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Best Local S
Matches 323
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Q86712;
01-NOV-1996
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Pfam; PF00069; pkinase; 1.

Pfam; PF02813; Retro M; 1.

ProDom; PD000001; EuK_pkinase; 1.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

ATP-binding; Transferase; 80649 MW; 84D2F6914EFEID63 CRC64;
                                                                                                         EMBL; S69372; AAC60725.1; -.
HSSP; P03322; 1A6S.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004028; Retro M.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                         evolution of distinct viral genomes of different transforming capacities."; Oncogene 9:1307-1320(1994).
EMBL; S69372; AAC60725.1; -.
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Polyprotein
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Hypothetical protein.
SEQUENCE 367 AA; 40163 M
                                                                                                                                                                                                                                 MEDLINE=94203659; PubMed=8152791;
Vennstrom B., Raynoscheck C., Jansson
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Viruses; Retroid virus
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01-NOV-1996
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                     Vennstrom B., Raynoscheck C., Jansson L., Doe Johnsson A., Beug H.;
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene evolution of distinct viral genomes carrying different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; S63372; AAC60727.1; -.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=94203659; Pubmed=8152791;
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Viruses; Retroid viruses; Retroviridae;
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IPR000719; Euk_pkinase
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Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00219; TYRKC; 1.

SMART; SM002107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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Q8WYV0;
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01-MAR-2002 (
01-JUN-2002 (
Hypothetical
P34659.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 9.3e-122;
3; Mismatches 112;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity
Matches 330; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002048; EF-hand.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00104019; YLP_motif.
Pfam; PF00069; pkinase; 1.
Pfam; PF000757; YLP; 2.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
                                                                                                                                                                              Q64895 PRELIMINARY;
Q64895;
Q64895;
Q1-NOV-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TREMBLrel. 21, La
Q1-JUN-2002 (TrEMBLrel. 21, La
Gag, V-erb-A, V-erb-B protein.
GAG, V-ERB-A, V-ERB-B.
                 SEQUENCE FROM N.A.

MEDLINE=90206603; PubMed=1969616;

Brunkin A., Jackson J., Bishop J.M.,

"Six amino acids from the retroviral
                                                                                                                  Avian erythroblastosis virus.
Viruses; Retroid viruses; Ret
NCBI TaxID=11861;
transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang Y., Zhou X.M., Zhar
Wan D.F., Gu J.R.;
"Novel human cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 412 AA; 4
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Submitted (NOV-2000) to the EMBL; AF318349; AAL55856.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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nilarity 80.5%;
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Pred. No. 2.1e-120;
5; Mismatches 22;
oncogene
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cCarley D.J., Schatzman
sne gag greatly enhance
v-erb-B.";
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Best Local S
Matches 358
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R PRINTS; PRO0047; STROIDFINGER.

R PPODOM; PD000001; Euk_pkinase; 1.

R ProDom; PD000001; Euk_pkinase; 1.

R ProDom; PD000035; Znf C4steroid; 1.

R PRODOM; PD000035; Znf C4; 1.

R SMART; SM0019; TYrKC; 1.

R SMART; SM0019; TYrKC; 1.

R SMART; SM0019; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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EMBL; X52211; CAA36459.1; JOINED.
HSSP; P10828; ZNLL.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR0017245; Tyr_pkinase.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 5:15-24(1990).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
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Pred. No. 1.6e
73; Mismatches
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-SRTPLLSSLSATSN---
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D Q85468

C Q85468;
C Q8546B;
JT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Avian Erythroblastosis virus (T834) v-erbB gene.
OS Avian erythroblastosis virus.
OC Viruses; Retroid viruses; Retroviridae; Avian type C
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InterPro; IPRO01245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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EMBL; X06943; CAA30024.; -.
HSSP; P11362; 1FGK.
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                              KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
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KGERLPOPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKWARDPPRYLVIOGDERMH
                                                                                                  YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE
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Pred. No. 3e-116;
0; Mismatches 121;
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                 A Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
A Schari K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Barownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaertts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danie Reiter J.L., Yee D., Lampland Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland Sinclair C.S., James C.I.
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Lampland A.L.,
Maihle N.J.;
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STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; PubMed=11217851;
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01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
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STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W.,
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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m S., Cross
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Best Local S
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EMBL; AF124513; AAD44149.1; -

EMBL; AF275366; AAG28047.1; JOINED.

EMBL; AF275365; AAG28047.1; JOINED.

EMBL; AF275365; AAG28047.1; JOINED.

EMBL; AK004944; BAB23680.1; -

EMBL; AK004941; BAB23680.1; -

EMBL; AK004911; BAB23662.1; -

MGD; MGI:95294; Egfr.

InterPro; IPR0002174; Furin-Tike.

Pfam; PF00757; Furin-like; 1.

Pfam; PF00757; Furin-like; 1.
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IMGENNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGC
                                                        CRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG
                                                                                     KLFGTPNQKTKIMNNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDCVSCQNVSRGRECVEK
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                   VKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGC
                                          CNILEGEPREFVENSECIOCHPECLPOAMNITCTGRGPDNCIOCAHYIDGPHCVKTCPAG
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Search completed: July 22, 2003, 09:00:39 Job time : 54.3575 secs

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Result
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ALIGNMENTS

RESULT 1 A24571 A; Molecule type: DNA A; Residues: 1-191 <T A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808 R;TA1, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D. Mol. Cell. Biol. 7, 2597-2601, 1987 A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for tra A;Reference number: 157622; MUID:87286898; PMID:3039351 A;Accession: 157622 A;Molecule type: mRNA
A;Residues: I-517,'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 740-910 <COUI>
A;Cross.references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989
A;Accession: B44188 A;Molecule type: mRNA
A;Residues: 1-1255 <YAM>
A;Residues: 1-1255 <YAM>
A;Residues: 1-1255 <YAM>
A;Cross references: GB.X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;Cross references: GB.X0363; N. Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epide
A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491 C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C;Accession: A24571; A25491; Ā44188; B44188; I59509; I57622
C;Accession: A24571; A25491; Ā44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Nature 319, 230-234, 1986
Nature 319, 230-234, 1986 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb_B-2 protein precursor; kinase-related transforming protein A;Status: translated from GB/EMBL/DDBJ A;Reference number: A44188; MUID:86070181; PMID:2999974 A;Accession: A44188 A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282 R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, A; Molecule type: DNA A; Residues: 737-1031 <SEM> A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growtle.Reference number: A24571; MUID:86118663; PMID:3003577 A;Molecule type: DNA A;Residues: 832-909 <REX> A;Status: translated from GB/EMBL/DDBJ A; Accession: A24571 promoter: evidence for multiple mechanisms for transcription
2; MUID:87286898; PMID:3039351 N.; Miyajima, N.; Saito, EGF receptor shares chrom J.; Seeburg, H e

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A;Cross-references: GB:M16792; NID:g183983; PI
C;Comment: Amplification and overexpression of
C;Genetics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17421.1-17421.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
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F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;22-65/Domain: EGF receptor extracellular domain repeat <EE1>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE2>
F;395-605/Domain: transmembrane #status predicted <TMM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;718-98J/Domain: protein kinase homology <KIN>
F;718-98J/Domain: protein kinase ATP-binding motif
F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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                                                                                CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY
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                                                           CSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY
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1; Mismatches
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A;Residues: 1-1260 cBAR>
A;Residues: 1-1260 cBAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Cross-references: EMBL:X03362; NID:g67410, E.M.; Okamura, T.; Smitl
A;Tidle: Direct DNA sequencing of the rat neu oncogene transmembrane dom
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane dom
2-thiazolyl]formamide or N-methyl-N-nitrosourea.
2-thiazolyl]formamide or N-methyl-N-nitrosourea.
A; Note:
C; Geneti
A; Gene:
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Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Accession: A24562
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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;558-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-93/Region: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted F;581/Binding site: phosphate (Thr) (covalent) #status predicted F;581/Active site: Lys #status predicted F;5882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
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C;Superfamil
C;Keywords:
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-011-1996 #sequence_revision 02-Jul-1996 #tex
C;Accession: I48161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.;
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A;Title: Cloning and activation of the Syrian hamster neu
A;Reference number: I48161; MUID:94193007; PMID:7908275
A;Accession: I48161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
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C;Genetics:
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                      KNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTD
                                                                     DPLNNFNNFTVSFWLRVPKVSASHLEQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH
                                                                                                            ELTYLPANATLSFLQDIQEVQGYMLIAHSQVRHVPLQRLRIVRGTQLFEDKYALAVLDNR
                                                                                                                             ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
KNNQLAPVDIDTNRSRACPPCAPACKDNHCWGASPEDCQTLTGTIAPRAVPAARARLPTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGDLVDAEEYLVPQQGFFSPDPTPGTGSTAHRRHRSSSTRSGGGELTLGLEPSEEGPPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMVKCWMIDSECRPRERELVSEFSRMARDPQREVVIQNEDLGPSSPMDSTFYRSLLEDDD
                                                                                                                                                                                                                                                                                                                           epidermal growth factor receptor;
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                 protein kinase
protein kinase
                                                                                                                                                                                                                                                                                                                                                                      GB:D16295; NID:g493236;
                                                                                                                                                                                                                                        86.5%;
                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                 ATP-binding
                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                        Score 5921.5; DB 2
Pred. No. 1.6e-235;
                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                  <KIN>
                                                                                                                                                                                                                                                                                                                                                                      PIDN:BAA03801.1;
                                                                                                                                                                                                                                                                                   motif
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                                                                                                                                                                                                                                                                                                                            protein
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                                                      YQDTVLWKDVFR
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                                                                                                                                                                                                                                                                                                                           homology
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                                                                                                   EYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
                                                                                                                                                                                    PQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENP
                                                                                                                                                                                                                                             LAPSEGAGSDVFEGELGMGATKGPQSISPRDLSPLQRYSEDPTLPLPTETDGYVAPLACS
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                                                                                                                                                                                                                                                                                                                                                       GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
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A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 «SIM»
R;Weber, W.; Gill, G.N.; Speiss, J.
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183;
A;Accession: A05281
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A;Molecule type: mRNA
A;Residues: 'RCAMRRA', 150-187, 'KSYIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-A;Residues: 'RCAMRRA', 150-187, 'KSYIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-A;Residues: 'RCAMRRA', 150-181, 'RY - A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF re R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, Science 224, 843-848, 1984
A;Call Residues: Raise amplificati A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615
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R;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672
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R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identificatio
A;Reference number: S30024; MUID:88217333; PMID:3329716
A;Accession: S30024
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A;Title: Characterization and sequence of the promoter region of Reference number: A25772; MUID:85270438; PMID:2991899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epidermal growth factor receptor precursor - human %;Contains: protein-tyrosine kinase (EC 2.7.1.112) C;Species: Homo sapiens (man) C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 C;Accession: A00641; A25772; $30024; A38672; A0064
                                                                                                                                                                                                                                                                                                            A;Experimental source: epidermoid carcinoma cell line A431 R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; waright, D.A.; Ca Biochem. Biophys. Res. Commun. 124, 125-132, 1984 A;Reference number: A23062; MUID:85046483; PMID:6093780
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A; Residues: 1-29 < HAL>
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A; Residues: 1-29 <HA2>
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A; Residues: 713-964 <LIN>
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;Species: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999
;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281;
;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.;
protein
),'S',32-51;454-
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A;Title: ATP-stimulated interaction between epidermal growth factor receptor and super A;Reference number: A38023; MUID:8419154; PMID:6325948
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C
Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain
A;Reference number: A3331; MUID:90003233; PMID:2790960
A;Contents: annotation; internalization signal
C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor
C;Genetics:
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:EGFR
A;Cross-references: GDB:120610; OMIM:131550
A;Gene: GDB:120610; OMIM:131550
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A;Title: Identification of residues in the nu A;Reference number: A60143; MUID:85182650; PM A;Accession: A60143
A;Molecule type: protein A;Residues: 740-744, 'X', 746-747 <RUS>R;Mroczkowski, B.; Mosig, G.; Cohen, S. Nature 309, 270-273, 1984
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                                                                              NIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENR
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9; Mismatches 351;
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epidermal growth factor receptor precuse-
c;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_chang
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
R;Luetteke, N C; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.;
Renes Dev. 8, 399-411, 1994
Genes Dev. 8, 399-412, 1994
Genes Dev. 8, 399-413, 1994
Genes Dev. 8, 399-413, 1994
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A;Molecule type: mRNA A;Residues: 1-1210 <LUE> A;Cross-references: GB:U

GB:U03425

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A; Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
C; Genetics:
A; Gene: EGFR
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor; kinase-related transforming protein; [F;1-24/7omain: signal sequence #status predicted <SIG>F;1-24/7omain: protein kinase homology <CKUM>F;1-2977/Domain: protein kinase homology <KUM>F;712-977/Domain: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697,1070,1071/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F;093/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: phosphate (Tyr) (covalent) #status experimental
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A;Rolecule type: DNA
A;Residues: 1-971'K',973-1210 <VER>
A;Residues: 1-971'K',973-1210 <VER>
A;Cross-references: EMBL:X78987; NID:948830; PIDN:CAA55587.
A;Cross-references: EMBL:X78987; NID:948830; PIDN:CAA55587.
R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor A;Reference number: 149643; MUID:93126380; PMID:7678348
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A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
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A;Accession: S45325
A;Status: preliminary
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R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
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A;Accession: S24942
A;Molecule type: mRNA
A;Residues: 969-971, 'K', 973-1115,'D'
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A;Title: Comparison of EGF receptor sequences as a guide A;Reference number: A43818; MUID:91232866; PMID:2030916
A;Accession: A43818
A;Molecule type: mRNA
A;Residues: 1-714 <AVI>
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                                     NQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDC
                                                                                                                                                                                              ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNFNN
                                                                                                               FTVSFWLRVPKVSASHLEQL--RSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKN
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                                                                                        PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPN
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780

768

661 649 720 708 361 350 421 410 481 470 531 530

1019

900 900 960 948

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A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, exp.
A;Reference number: A27720; MUID:88261272; PMID:3260329
A;Accession: A27720
A;Molecule type: mRNA
A;Residues: 1-123 <LAX>
A;Cross-references: GB:M20386
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.
Cell 41, 719-726, 1985
Cell 41, 719-726, 1985
A;Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA proceasion: A00643; MUID:85228222; PMID:2988784
A;Accession: A00643
A;Accession: A00643
A;Accession: A00643
A;Cross-references: GB:M10066
C;Genetics:
A;Genetics:

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F;727-735/Region: protein kinase ATP-binding motif
F;727-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635,635/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;192,650/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #st
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #st
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F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-1223/Product: epidermal growth factor receptor #s
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chicken N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-1995 #sequence_revision 05-May-19
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RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYIS
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48.0%; Pred. No. 1.1e-119;
tive 175; Mismatches 351;
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GNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                                                           NNISLTAISKLPMDSRYQNSHSTAVDNPEYL-
                                                                                                                                                                                                                    EAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSE 1129
                                                                                                                                                                                                                                                     MEEEDMEDIVDADEYLVPHQGFF-----
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                            RGAPPSTFKGTPTAENPEYLGLDVP 1260
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epidermal growth factor receptor, HER4 - human (Species: Homo sapiens (man) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text C;Accession: A47253 #sequence_revision for C.S.; Green, R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993 A;Title: Ligand-specific activation of HER4/p180erbB4, a

18-Nov-1994 #text_change

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fourth member of the Carlton, G.W.; 18-Jun-1999

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A;Reference number: A47253; MUID:93189574; PMID:8383326
A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-1308 <PLO>
A;Residues: 1-1308 <PLO>
A;Cross-references: GB:LO7868; NID:9337359; PIDN:AAB59446.1; PID:9337360
A;Mote: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
F;716-991/Domain: protein kinase homology <KIN>
F;724-732/Region: protein kinase ATP-binding motif
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                                                        ANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDL 828
                                                                                                                             SGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPK
                                                                                                                                                                                  QHAR-TPL--IAAGVIGGLFILVIVGLTFAVYVRRKSIK-KKRALRRFL-ETELVEPLTP
                                                                                                                                                                                                                     AEQRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP 708
                                                                                                                                                                                                                                                                                                                             RGRICIESCNLYDGEFREFENGSICVECDPQCEKWEDGLLTCHGPGPDNCTKCSHFKDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                        FVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFL 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAW 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHRECAGGCSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVWVSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEITS
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LNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGG
                                ANVEFMDEALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLL
                                                                                                        SGTAPNQAQLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETVKIPVAIKILNETTGPK
                                                                                                                                                                                                                                                         NCVEKCPDGLQGANSF--IFKYADPDRECHPCHPNCTQGCNGPTSHDCIYYPWTGHSTLP
                                                                                                                                                                                                                                                                                          FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC-----P
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                                                                                                                                                                                                                                                                                                                                                                                                         YYHTINWTTLFSTINORIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKKCPHNFV-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASC
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Pred. No. 2.8e-115;
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A;Title: A;Refere A;Access	A;Molecu A;Residu A;Cross - R;Adam, Oncogene	A;Tit	R; Witt	C;Speci C;Date:	S06142 protei N;Alte	RESULT	Db .	δ	DЬ	Ş	οь	Ş	Дb	ş	DЪ	Ş	DЬ	Q	Db	Ş	40	Ş	Db
Transcript nce number ion: \$1380	A;MoLecule type: DNA A;Residues: 1-1166 <wit> A;Residues: 1-1166 <wit> A;Cross-references: EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291 R;Adam, D.; Maeueler, W.; Schartl, M. Oncogene 6, 73-80, 1991</wit></wit>	e: Novel putati rence number: S ssion: S06142		iphophorus maculatus (southern ep-1999 #sequence_revision 10-5	n-tyr rnate	ži oo	1252 TLQHPDYLQEYSTKYFYKQNGRIRPIVAENPEYL 1285	1238 APPSTFKGTPTAENPEYL 1255	1195PPKAEDEYVNEPLYLNTFANTLGKAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRS 1251	1212 QPHPPPA	1168ENPFVSRR	1152 RPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAAP 1211	1109 GTLRKPVAPHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVE- 1167	1099 GAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDV 1151	1049 GHSPPPAYTPMSGNQFVYRDGGFAAEQGVSVPYRAPTSTIPEAPVAQGATAEIFDDSCCN 1108	1068 GLEPSBEEAPRS	1001 SKFFQNLLDEEDLEDMMDAEEYLVP-QAFNIPPPIYTSRARIDSNRSEI 1048	1008 STFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTL 1067	941 QPPICTIDVYMYMVKCWMIDADSRPKFKELAAEFSRWARDPQRYLVIQGDDRMKLPSPND 1000	949 OPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPORFVVIQNED-LGPASPLD 1007	881 KMPIKWMALECIHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLP 940	889 KVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLP 948	: :

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N;Alternate names: epidermal growth factor receptor homolog; kinase-related transfo C;Species: X;Dhophorus maculatus (southern platyfish)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 18-Feb-2000
C;Accession: S0142; S13809
C;Accession: S0142; S13809
A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing TA;Reference number: S06142; MUID:90015140; PMID:2797166
A;Accession: S06142
A;Molecule type: DNA
A;Reference number: S06142; MUID:90015140; PMID:2797166
A;Accession: J1166 our of the melanoma inducing Xmrk oncogene in Xipho
A;Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xipho
A;Coss-references: EMBL:X16891; NID:365290; PIDN:CAA34770.1; PID:365291
A;Reference number: S13807; MUID:91125882; PMID:1846957
A;Accession: S13809
A;Status: preliminary; translation not shown
A;Residues: 921-1025, NY, 1027-1098, A', 1100-1166 <ADA-A;Coss-references: EMBL:X56319; NID:365284; PIDN:CAA39763.1; PID:365285
A;Gene: mxk
A;Residues: 821-1025, NY, 1027-1098, A', 1100-1166 <ADA-A;Coss-references: EMBL:X56319; NID:365284; PIDN:CAA39763.1; PID:365285
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244 EQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVT	OY 185 LALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCH 243 ::	QY 128 NFTVSFWLRVPKVSASH-LEQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQ 184	QY 68 NASLSFLQDIQBVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNFN 127	Qy 10 GLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67	Query Match 35.3%; Score 2418.5; DB 2; Length 1342; Best Local Similarity 40.4%; Pred. No. 5.2e-92; Matches 533; Conservative 192; Mismatches 454; Indels 141; Gaps 34;	; phosphotransferase n: protein kinase homology <kin></kin>	A;Gene: GDB:ERBB3; HER3 A;Cross-references: GDB:119880; OMIM:190151 A;Map position: 12q13-12q13 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase home	ference	A.Accession: I59164 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Wolecule type: mRNA	Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990 A;Title: Molecular cloning and expression of another epidermal growth factor receptor A;Reference number: I59164; MUID:90311312; PMID:2164210	REAP BERN29366	A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epiderma A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Accession: A36223 A;Status: preliminary	C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 C;Accession: A36223; I59164 R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A. Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989	ESULT 9 36223 inase-re	1140		Qy 1180 SPGKNGVVKDVFAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAP 1239	1133 YVAPLTCSPQPEYVNQPDVRPQPPSPREGPLP-AARPAGATLERAKTL		Qy 1074 EEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDG 1132

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  RHSP-
                          GAAPOPHPPPAFSPAFDNLYYWD------
                                                      EEDVNGYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED-----
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                                                                                                                                                                   RPRGSQSLLSPSSGY-MPMNQGNLGESCQESAVSGSSERCPRPVSLH-----PMPRGCL
                                                                                                                                                                                               EEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHD-PSPLQRYSEDPTVPLP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVARCPSGVKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGCPAEQRA----SPL
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                                                                                                                                        -SETDGYVA----
                                                                                 -----LPAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEYLTPQG
PHPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYM
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                                                                                                                                        ----PLTCSPOPE----YVNOPDVRPOPPSPREGP---
                          QDPPERGAPPSTFKGTPTAENPEYL
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RESULT JC4387

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epidermal growth factor receptor homolog precursor - rat

NyAlternate names: ErbB3 protein; HER3 protein

C;Species: Rattus norvegicus (Norway rat)

C;Bate: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998

C;Accession: JC4387

R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Koland, J.G.

Gene 165, 279-284, 1995

A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant |
A;Title: Cloning of the rat ErbB3 cDNA and characterization of the recombinant |
A;Reference number: JC4387; MUID:96096535; PMID:8522190

A;Reference number: JC4387; MUID:96096535; PMID:8522190

A;Residues: 1-1339 <HEL>
A;Coss-references: GB:U29339; NID:g915389; PID:g915390

A;Experimental source: liver

A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT for C;Comment: This protein is a functional heregulin receptor that transduces sign
C;Gene: ErbB3

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinases; Syndonin: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Product: epidermal growth factor homolog #status predicted <MAT>
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Best Local Simi
Matches 523;
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;713-721/Region: protein kinase ATP-binding motif
;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
AHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSC--VDLDDKGCPAE
                                                                                                              CVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVAC
                                                                                                                                                                               SANQQLCYHHSLNWTRLLRGPSEERLDIKYDRPLGECLAEGKVCDPLCSSGGCWGPAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYGGVCVASCPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKG
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                                                                                                                                                                                                                                                                                      LNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRVYI
                                                                                                                                                                                                                                                                                                                                                                                           -SRYQTVDSSNIDGFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVREITGY
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(Tyr)

F;229/Active

site:

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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus
N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 11-Jun-1999
C;Accession: B00643; A00643
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
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                       SPAFDNLYYWDQ-----
                                                                                                              RYSEDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE 1174
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KTVFESSPYWIQSGNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                                                                                                 RYSSDPTGNFLEESIDDGFL-----PAPEYVNQ--LMPKKPS-----
                                                                                                                                                                         GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
                                                                                                                                                                                                                                                                                                    YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE
                                                 -TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-
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Pred. No. 1.4e-65;
D; Mismatches 137
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                                                                     --AFGGAVENPEYLTPQGGAAPQPHPPPAF
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A;Residues: 1-604 <YAM>
A;Cross-references: GB:KO1216; NID:g209676; PIDN:AAA42400.1; PID:A;Cross-references: GB:KO1216; NID:g209676; PIDN:AAA42400.1; PID:GEbuire, B:; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.: Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosis virus A;Reference number: A38022; MUID:84223957; PMID:6328658
                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain c;Species: avian erythroblastosis virus C;Date: 18-Apr-1984 #Bequence_revision 18-Apr-1984 #text_change 11-Jun-1999 C;Accession: A00644; A38022 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K. Cell 35, 71-78, 1983 A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene A;Reference number: A00644; MUID:84026539; PMID:6313229 A;Molecule type: DNA A;Molecule type: DNA
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A;Accession: A38022
A;Molecule type: DNA
A;Residues: 1-28, 'W', 30-139, 'F', 141-145, 'V', 147-152 < A;Residues: 1-28, 'W', 30-139, 'F', 141-145, 'V', 147-152 < A;Residues: 1-28, 'W', 30-139, 'F', 120-145, 'V', 147-152 < A;Rene: erbs
C;Genetics: A;Gene: erbs
C;Superfamily: epidermal growth factor receptor; protoc;Superfamily: epidermal growth factor receptor; protoc;Reywords: ATP; oncogene; phosphotransferase; transfer;130-395/Domain: protein kinase homology < KIN-F;138-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted
      epidermal growth factor receptor - fruit fly (Drosophila melanogaster) N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun C;Accession: A00640; A38021 C;Accession: A00640; A38021 C;Schlessinger, J.; Shilo, B.Z.
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                                                                                                                                                                                                                                                                                                                                                                                          LPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGK 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICTIDVYMIMVKCWMIDADSRPKFRELIAEFSKWARDPPRYLVIQGDERMHLPSPTDSKF
                                                                                                                                                                                                                                                                           - VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL---
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GB:K02006
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Pred. No. 4.8e-63;
6; Mismatches 128
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    Schlessinger,
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transforming protein; tyrosine-specific
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                                    #text_change 11-Jun-1999
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                                    QRGRLLGSWHGSVPYLQELQFQWHLHRRLWLYIQVSINSTQDKSNEHQLTDACYSPSVPT
                                                                                                               SNIRWPAIQKEPEQKVWVNENLRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSV
                                                                                                                                                   HTVPWDQLFRNPHQALLHTANRPEDEC
                                                                                                                                                                                          FRILSYFRILETIHGRQLMESMFAALAIVKSSLYSLEMRILKQISSGSVVIQHIRDLCYV
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                                                                                                                                                                                                                                                                                           CKKIFGSLAFLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDS
                                                                                                                                                                                                                                                                                                                                                    DNGACVRSCPQDKMDKGGE-----CVPCNGPCPKTCPGVTVLH-----AGNIDSFRN
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DLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAP 135

194

540

483

510 420 424

360

372

253

300

312

194

Mismatches 414;

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A;Cross references: FlyBase:FBgn0003731

A;Map position: 2 57F
C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATF; autophosphorylation; duplication; glycoprotein; phosphop F;1-732/Domain: extracellular #status predicted <EXT>F;733-764/Domain: intracellular #status predicted <TMM>F;765-1330/Domain: intracellular #status predicted <INT>F;608-1072/Domain: intracellular #status predicted <INT>F;816-824/Region: protein kinase homology <KIN>F;816-824/Region: protein kinase ATP-binding motif F;212,300,324,363,518,688,695,700/Binding slite: carbohydrate (Asn) (coval F;744/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta F;843/Active site: Lys #status predicted
F;1181/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
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A;Accession: A00640
A:Molecular
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A;Title: A Drosophila genomic sequence with A;Reference number: A38021; MUID:85137938; FA;Accession: A38021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 'A',832-866,'V',868-943,'QTDSLVK' <WAD>
A;Cestdues: 'A',832-866,'V',868-943,'QTDSLVK' <WAD>
C;Comment: This sequence is tentative because the introns have not been
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A; Residues: 1-1330 <LIV>
A; Cross-references: EMBL: K03054
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A; Title: The Drosophila
   24.2%;
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Score 1655.5; DB 1; Length 1330 Pred. No. 9.2e-61;
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PMID:2983232
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RESULT 14

$35745

$35745

protein-tyrosine kinase (EC 2.7.1.112) erbB - avi
C;Species: avian erythroblastosis virus
C;Date: 03-Mar-1994 #sequence_revision 26-May-19;
C;Accession: $35745

R;Vennstroem, B.
submitted to the EMBL Data Library, March 1993
A;Reference number: $35743
A;Accession: $35745
A;Molecule type: DNA
A;Residues: 1-544 <VEN>
A;Cross-references: EMBL:X12707
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                                                                                                                                                avian erythroblastosis
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RESULT 15
S00727
S00727
kinase-related transforming protein (erbB) (EC 2.7
c.Species: avian erythroblastosis virus
C.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989
C.Accession: S00727
R.Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, 7
Oncogene Res. 1, 265-278, 1987
A.;Title: Common site of mutation in the erbB gene
A.;Reference number: S00727; MUID:88217326; PMID:28
A.;Accession: S00727
A.;Molecule type: DNA
A.;Residues: 1-545 <SCO>
A;Cross-references:
C;Genetics:
A;Gene: erbB
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A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homol
C;Superfamily: epidermal growth factor receptor; protein kinase homol
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein;
P;135-400/Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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70; Mismatches
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                                                                                         erbB gene of avian
26; PMID:2897102
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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; phosphotransferase F;135-400/Domain: protein kinase homology <KIN>F;143-151/Region: protein kinase ATP-binding motif
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run 92: July 22, 2003, 08:12:49; Search time 10.2793 Seconds (without alignments) 5088.033 Million cell updates/sec

Title: Perfect score: SEQ4-103-117-14 6847 1 MELAALCRWGLLL

Sequence: MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261

Scoring table: BLOSUM62 Gapop 10.0 ,

Gapext 0.5

112892 seqs,

41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pfam; PF01030; Recept L domain; 2.

Pfam; PF01030; Recept L domain; 2.

Pfam; PF02757; YLP; 2.

ProDom; PD000001; Buk pkinase; 1.

ProDom; PM00201; FU; 3.

SMART; SM00261; FU; 3.

SMART; SM00261; FU; 3.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR0014019; YLP_motif.
Pfam; PF00069; pkinase; 1.
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RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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"An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
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TISSUE-Neuroblastoma;
TISSUE-Neuroblastoma;
MEDLINE-86118662; PubMed-3945311;
Bargmann C.I., Hung M.-C., Weinberg
"The neu oncogene encodes an epidern
                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p06494;
p06494;
p01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat Receptor protein-tyrosine kinase erbB-2 pre (p185erbB2) (NEU proto-oncogene) (C-erbB-2)
receptor-related protein).
                                                                                                                                                                                                                           protein
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                                                                                                MEDLINE=91222560;
                                                                                                                       SEQUENCE OF 852-905 FROM N.A. TISSUE=Sciatic nerve;
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1-tyrosine kinase erbB-2 precursor (EC 1
1 proto-oncogene) (C-erbB-2) (Epidermal protein)
                                                                                                PubMed=2025425;
                                                                                                                                                                                                                                               epidermal
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Sciurognathi; Muridae; Murinae; Rat
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MEDLINE=92155181; PubMed=1346763;
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ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 1
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, 1
ALPHA AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protei
tyrosine phosphate.
Tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOME
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
RESIDUES (BY SIMILARITY).
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; X03362; CAA270 A24562; TVRTNU. P11362; 1FGK domain.

Pfam; PF02757; YLF; 2.
Pfam; PF02757; YLF; 2.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00216; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE DOM; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transmembrane; GlycoproteIn; Multigene family; Receptransmembrane; GlycoproteIn kinase; ATP-binding; InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP_motif.
Pfam; PF00059; pkinase; I.
Pfam; PF00059; pkinase; I.
Pfam; PF000757; Purin-like; 1.
Pfam; PF01030; Recep_L domain; 2.
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(BY SIMILARITY) PROTEIN-TYROSINE Receptor; eptor; Signal;
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                                                                                                                                                                                                                                                                                                                                                             CCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPLNNFNNFTVSFWLRVPKVSASHLEQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFH
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                                                                                                                                 FLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDP
                                                                                                                                                                   CFVHTVPWDQLFRNPHQALLHSGNRPEEDLCVSSGLVCNSLCAHGHCWGPGPTQCVNCSH
                                                                                                                                                                                 | CFVHTVPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHCWGPGPTQCVNCSQ
                                                                                                                                                                                                                   WPDSLRDLSVFQNLRIIRGRILHDGAYSLTLQGLGIHSLGLRSLRELGSGLALIHRNAHL
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nilarity 87.1%;
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Pred. No. 1.8e-311;
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X MEDLINE 94193007; PubMed 7908275;
A Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
A Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
A Yamazaki Y., Ishikawa T.;
T "Cloning and activation of the Syrian hamster neu proto-oncogene.
I Gene 140.251-255 (1994).
C -!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLE
C ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS
C POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF
C POTENTIAL AND AMPHIREGULIN (BY SIMILARITY).
C -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
C C -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
C -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
C -!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                        Q6053;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor
(p185erbB2) (NEU proto-oncogene) (C-erbB-2).
ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                Mesocricetus auratus
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERB2
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Mesocricetus.
NCBI_TaxID=10036;
[1]
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   SUBCELLULAR LOCATION:
PTM: LIGAND-BINDING IN
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Chordata; Craniata; Vertebrata; |
Rodentia; Sciurognathi; Muridae;
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INCREASES
membrane protein
S PHOSPHORYLATION
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Cricetinae;
   TYROSINE
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Length

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Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF02757; YLP; 2.
Pfo20m; PF020001; Dk pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
Transmembrane; Glycoprotein, Kinase; ATP-binding; Phosphorylation;
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proto-oncogene; SIGNAL 1
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InterPro;
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InterPro;
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SIMILARITY:
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P11362; 1FGK.
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                                     LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=84219729; PubMed=6328312;

Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,

Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,

Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;

"Human epidermal growth factor receptor cDNA sequence and aberrant

expression of the amplified gene in A431 epidermoid carcinoma cells.";

Nature 309:418-425(1984).
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                                                                                                                  Tlekis J.V., Gariti J., Niederberger "Expression of a truncated epidermal protein (TEGFR) in ovarian cancer."; Gynecol. Oncol. 65:36-41(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97078686; PubMed=1
Reiter J.L., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
   MEDLINE=21100872;
                              TISSUE=Placenta;
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         MEDLINE=97256547; PubMed=9103388;
                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
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Reiter J.L., Threadgill D.W., I Lampland A.L., Balasubramaniam Maihle N.J.;
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Nature 309:806-810(1984).
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Lin C.R., Chen W.S., Kruiger W., Stolarsky
Evans R.M., Verma I.M., Gill G.N., Rosenfe
"Expression cloning of human EGF receptor
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-29 FROM N.A.
MEDLINE=88217333; PubMed=3329716;
Haley J.D., Whittle N., Bennett P.,
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1028-1210 FROM N.A. MEDLINE=85046483; PubMed=6093780; Simmen F.A., Gope M.L., Schulz T.
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Schehl Sinclair C., Pearsall R.S.,
Balasubramaniam S., Crossley T.D.,
 RECEPTOR ACTIVITY.
MEDLINE=84191554; PubMed=6325948;
MYCOZROWSKI B., Mosig G., Cohen S
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                                                                                                  Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merl "Characterization and sequence of the promoter repidermal growth factor receptor gene.", proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985)
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O'Malley B.W
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Xu Y.H., Ishii S., Clark A.J.L.,
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                                                        Submitted
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                                                                                                                                                                                                              "Contributory effects of de
                                                                                                                                                                                                                                    SEQUENCE OF 1-29 FROM N.A. MEDLINE=91107677; PubMed=1988448;
                                                                                                                                                                                                                                                                    "The human EGF receptor gene: structure identification of sequences regulating Oncogene Res. 1:375-396(1987).
                                                                                                                                                                                                                                                                                                        Waterfield M
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Roe B.A., Merlino (
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m S., Cross
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Yee D., Lampland
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                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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"All autophosphorylation sites of epidermal growth factor (EG receptor and HERZ/neu are located in their carboxyl-terminal Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
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MEDLINE=96398132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V.,
Smith K.D., Davies M.J., Bailey D., Renouf D.V.,
"Analysis of the glycosylation patterns of the ex
"Analysis of the factor receptor expressed in
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                                                                                                                                                                                                                                                                                                                                                    u. Rev. Biochem. 56:881-914(1987).

FUNCTION: Receptor for EGF, but also for other members of the FEMCTION: Receptor for EGF, but also for other members of the Femily, as TGF-alpha, amphiregulin, betacellulin, heparin-bindi EGF-like growth factor. GP30 and vaccinia virus growth factor. involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                            expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (struncated isoform/TEGFR, 3/p110 and 4; are alternative splicing.
TISSUE SPECIFICITY: Expressed in placenta.
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ry fibroblasts.";
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309:270-273(1984).
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                                              EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR
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                                                                        SEQUENCE FROM N.A.
STRAIN-B6/C3; TISSUE=Liver;
STRAIN-B6/C3; TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu T Jenkins N.A., Lee D.C.;
"The mouse waved-2 phenotype result receptor tyrosine kinase.";
Genes Dev. 8:399-413(1994).
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Q01279;
Q1-FEB-1996
01-FEB-1996
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
      Avivi
                                                                                                                                                                                                                           STRAIN=BALB/c;
Hibbs M.L.;
                                                                                                                                                                                                                                                                                  MEDLINE=93126380; PubMed=7678348; Paria B.C., Das S.K., Andrews G.K., Dey S.K.; Paria B.C. Das S.K., Andrews G.K., Dey S.K.; Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                SECUENCE OF 1
TISSUE=Brain;
                                                                                                                                                                                                                                                        SEQUENCE
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                  MEDLINE=91232866;
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7:1957-1962(1992).
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   PubMed=2030916;
Ullrich A., Sch
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Last annotation update)
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Sciurognathi; Muridae;
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Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain
ProDom; PD000001; Buk pkinase
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
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PROSITE; PS00109;
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SM00261; FU; 3. SM00219; TyrKc; 1

Euk_pkinase;

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PS50011;

PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_DOM; 1.
YCoprotein; Receptor; Signal; Transferycoprotein; Receptor; Phosphorylation;

Signal; Transferase;

kinase;

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CYTOPLASMIC POTENTIAL EXTRACELLULAR POTENTIAL.
EPIDERMAL GROWTH

(POTENTIAL)

(POTENTIAL)

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Oncogene 6:673-676(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisinger D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparison of EGF receptor
                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane
MISCELLANEOUS: Binding of EGF to the I
; X78987; CAA55587.1; -
; U03425; AAA17899.1; -
; X59699; CAA42219.1; -
; L06864; AAA53029.1; -
; Z12668; CAA78249.1; -
>, P11362; 1FGK.
                                                                                                                                                                                                                                                                                                 synthesis, and cell proliferation. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                    SUBCELLAHLAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to
dimerization, internalization of the EGF-receptor compl
induction of the tyrosine kinase activity, stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitted (JUN-1992) to the EMBL/GenBank/DDBJ databases. FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEBARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY)
                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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B4 HUMAN STANDARD; PRT; 1308 AA.

O15303;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precurse (p180erbB4) (Tyrosine kinase-type cell surface in ERBB4 OR HER4.
SEQUENCE FROM N.A. (ISOFORM JM-A)
TISSUE-Breast carcinoma;
MEDLINE-93189574; PubMed-8383326;
Plowman G.D., Culouscou J.-M., Wh
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HE
                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
[1]
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PFGAM; PFG1030; Recep L domain; 2.

Pfam; PFG1757; YLP; 2.

Pfam; PFG2757; YLP; 2.

PFGDOM; PDG00001; Euk_pkinase; 1.

SMART; SM00261; FU; 4.

SMART; SM00261; FU; 4.

SMART; SM00261; PROTEIN KINASE ATP; 1.

PROSITE; PSG0109; PROTEIN KINASE DOW; 1.

PROSITE; PSG0011; PROTEIN KINASE DOW; 1.

Transmembrane; Glycoprotein; Multigene fami
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MEDLINE=97476287; PubMed=9334263;
Corfas G., Paul S., Choi C.J., Rio C.,
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DOMAIN
                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07868; AAB59446.1;
HSSP; P11362; 1FGK.
Genew; HGNC:3432; ERBB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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J. Biol. Chem.
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SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A, (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPILICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESED IN
CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.

KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM,
PITULTARY, SPLEEN, TESTIS AND BREAST: LOWER LEVELS IN THYMUS,
LUNG, SALIVARY GLAND, AND PANCREAS.

LUNG, SALIVARY GLAND, AND PANCREAS.

PROCESSED FOR THYMUS,
DESCRIPTION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-
2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELIULIN AND
NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.
NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF
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                                                                                                                                                                                                                                                                                                                                ; IPRO00494; EGFR_L domain.
; IPRO00719; Euk pkinase.
; IPRO02174; Furin-like.
; IPR001245; Tyr_pkinase.
; IPR004019; YLP_motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
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                                                                                                                                           Tyrosine-protein
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. Sci. U.S.A. 90:1746-1750(1993).
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        POTENTIAL.
RECEPTOR PROTEIN-TYROSINE K
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
CYS-RICH.
CYS-RICH.
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                                                                                                                                           kinase;
                                                                                                                                      e family; Receptor; Signal;
ATP-binding; Phosphorylation;
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EMBL; AF041838; AAD08899.1; -.
EMBL; U5253; AAC53051.1; -.
HSSP; P11362; IFGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0012174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
   Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Pkinase; 1.
Pfam; PF01030; Recep L domain;
Pfam; PF02757; YLP; 2.
PRINTS; PR00109; TYRKINASE.
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Euk pkinase;

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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley; TISSUE-Spinal cord;
STRAIN-Sprague-Dawley; TISSUE-Spinal cord;
MEDLINE-97184212; PubMed-9030624;
Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbe
"Expression of neuregulins and their putative receptors,
ErbB3, is induced during Wallerian degeneration.";
J. Neurosci. 17:1642-1659(1997).
J. Neurosci. 17:1642-1659(1997).
ACTIVATED BY NEUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Neuregulins promote survival and growth of cardiac Persistence of ErbB2 and ErbB4 expression in neonata ventricular myocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao Y.-Y., Sawyer D.R., Bal
Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last Receptor protein-tyrosine k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuron 6:691-704(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in the vertebrate nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91222560;
Lai C., Lemke G.;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                            RECEPTORS (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING
TISSUE SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTI
OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN T
RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY,
HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine phosphate.
SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION. NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN (BY SIMILARITY). CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                              PTM: LIGAND-BINDING INCREASES RESIDUES (BY SIMILARITY).
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Rodentia;
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Sciurognathi; Muridae;
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SMART; SM00219; TyrKC; 1.
PROSITE; PRO0107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation.
POTENTIAL.
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610; Conserv
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                               LNYRKDGNFG
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%; Pred. No. 9.46
192; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR PROTEIN-TYROSINE KEXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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Pfam; PF00069; pkinase; I.
Pfam; PF000757; Furin-like; 1.
Pfam; PF001030; Recep L. domain; 2
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1
SMART; SM00261; FU; 5.
SMART; SM00219; TYRC; 1.
SMART; SM00219; TYRC; 1.
                     SMART; SM00219; Tyrkc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS00101; PROTEIN KINASE DOM;
Transmembrane; Glycoprotein; Receptor;
Tyrosine-protein kinase; ATP-binding;
SIGNAL 1 25
                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90015140; PubMed=2797166; Wittbrodt J., Adam D., Malitschek B., Maueler W., Telling A., Robertson S.M., Schartl M.; "Novel putative receptor tyrosine kinase encoded inducing Tu locus in Xiphophorus.";
                                                                                                                                                                                                                                                                                                     EMBL; X16891; CAA34770.2; PIR; S06142; S06142.
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Submitted (JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                    InterPro;
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Eukaryota; Metazoa; Chordata; Craniata; Ver
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15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE
CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + prot
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
IPR002290; Ser thr pkinase.
IPR001245; Tyr_pkinase.
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(Rel. 40, Last sequence up)
(Rel. 41, Last annotation)
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PROTEIN KINASE TYR; 1.
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PROTEIN KINASE DOM; 1.
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; Signal; Transferase;
       RECEPTOR PROTEIN-TYROSINE
                                 Phosphorylation; Proto-oncogene
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YLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLAL
                          SLSNTIAVNSTNIRSFSNCTKINGDIILNRNSFEGDPHYKIGTMDPEHLWNLTTVKEITG
                                          HLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITG
                                                                                 YTFGAACVKECPSNYVVTE-GACVRSCSAGMLEVD
                                                                                                         YTFGASCYTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGME
                                                                                                                                      GPKPIDCCNEHCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIK
                                                                                                                                                                GPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGR
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CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL).
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No. 3e-137;
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                             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC (C-erbB3) (Tyrosine kinase-type cell surface receptor
                                                                                           HUMAN
ERB3_HUMAN
 Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                            ERBB3 OR HER3.
                                                                                   P21860;
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                                                                                           STANDARD;
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  Primates;
          Chordata;
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Craniata; Vertebrata; Catarrhini; Hominidae;
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HER3).
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
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InterPro; IPR001245; Tyr pkinase; 1.
InterPro; IPR00130; Recep L domain; 2.
InterPro; IPR00130; Euk pkinase; 1.
InterPro; IPR00130; Euk pkinase; 1.
INTERPROSITE; INTERPRO; INTERPRO; INTERPROSITE; PR00101; INTERPROSITE; PR00101; INTERPROSITE; PR00101; INTERPROSITE; PR0011; INTERPROSITE; PS00109; INTERPROSITE; PS00109; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INTERPROSITE; INT
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EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB26935.1; -.
PIR; AA6223; A36223.
HSSP; P11362; 1FGK.
Genew; HGNC:3431; ERBB3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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Biochem. Biophys. Res. Commun. 192:1189-1197(1993)
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULIN
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine =
-!- CYTALYTIC HETERODIMER WITH EACH OF THE OTHER ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=90311312; PubMed=2164210;
Plowman G.D., Whitney G.S., Neubauer
Todaro G.J., Shoyab M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 190151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT FORM).

SECRETED (SHORT FORM).

-I- ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AN SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

-I- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITS SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

-I- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

-I- DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.

-I- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93282822; PubMed=7685162;
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                     PRT;
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15-JUN-2002
15-JUN-2002
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EMBL;
HSSP;
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Hellyer N.J., Koland
Submitted (DEC-2001)
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STRAIN-Sprague-Dawley; TISSUE=Liver;
MEDLINE=96096335, PubMed=8522190;
Hellyer N.J., Kim H.-H., Greaves C.H.
"Cloning of the rat ErbB3 cDNA and cleaned in the combinant protein.";
Gene 165:279-284(1995).
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Sci
MEDLINE=97184212; PubMed=9030624;
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                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS CATALYTIC ACTIVITY: ATP + a protein tyrosine = I
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U52530; AAC53050.1;
P11362; 1FGK.
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
IPR001245; Tyr pkinase.
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(Rel. 41, Last seq
(Rel. 41, Last ann
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oa; Chordata;
ia; Rodentia;
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annotation update)
kinase erbB-3 precursor
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Sciurognathi; Muridae;
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Murinae; Rattus
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LYISAWPDSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALI
                                                                                                                                                                                PNPNQCCHDECAGGCSGPQDTDCFACRRFNDSGACVPRCPEPLVYNKLTFQLEPNPHTKY
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P04412; O61601; Q9W2G0; P81868;
13-AUG-1987 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC (Gurken receptor) (Torpedo protein) (Drosophila EGFR OR TOP OR C-ERBB OR DER OR CG10079
BUSEK UK 10F OR CHANGESTER (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., & Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., & George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., & George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., & George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., & George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., & George Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G., RA Burandon R.C., Baldwin D., Bahadari D., Bothinkoch C., Baldwin D., Ra Ballew R.M., Babla A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Babla R., Banck J., Brandari D., Bothier A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Delter S.M., RA Ghodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Goder C., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Alashi N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howland T.J., Wei M.-H., Ibeywam C., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobary C., Morris J., Moshrefi A., Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden K.A., Nixon K., Nusskern D.R., Paeleb J.M., Nelson D.L., Ra Raineri K., Kernika R., Venter E., Wang A.H., Mang X., Weis
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ANALYSIS.
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Lesokhin A.M., Yu S.-Y., Katz J., Baker N.
"Several levels of EGF receptor signaling
specification in wild-type, Ellipse, and n
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g during photoreceptor
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Williams S.M., Wood
Ye J., Yeh R.-F., I
Zheng X.H., Zhong I
Gibbs R.A., Myers I
                                                                                                                EMBL;
                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"A Drosophila genomic sequence with homology to human epidermal growth factor receptor.";
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MEDLINE=85137938; PubMed=2983232;
                                                                                                                                                                                                                                                                                                                                                  between
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FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAWHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAWHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL TIRSUES, AND FOR THE DETERMINATION OF HOTH THE ANTERO-POSTERIOR AND DORSO-VENTEAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FATES.
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SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE I
                                                                                                                                                                                                                                                                                                                        European
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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AF052754; AAC08536.1; -...
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AF052754; AAC08535.1; -...
AF052752; AAC08535.1; -...
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K03054; AAA51460.1; -...
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K03416; AAA50965.1; -...
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K03418; AAA50461.1; -...
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AF109078; AAD26134.1; -...
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L09078; AAD26132.1; -.
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receptor-tyrosine kinases.";
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InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR0007174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF000757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00219; TYRKC; 1.
SMART; SM00219; TYRKC; 1.
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EMBL; AF109078; AAD26133.1; JG
EMBL; AF109079; AAD26130.1; JG
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EMBL; AF109080; AAD26132.1; JG
EMBL; AF109080; AAD26135.1; JG
EMBL; X7091080; CAA56523.1; JG
EMBL; X70919; CAA55522.1; JG
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PS00109; PROTEIN KINASE TYR; 1.
PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                           SDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVG
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IFGSLAFLPESFDG--DPASNTA-----PLQPEQLQVFETLEEITGYLYISAWPDSLPD
                                         ACVRSCPQDKMDKGGE----
                                                                            SCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKK
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ATP (BY SIMILARITY).
BY SIMILARITY.
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PRINTS; PR00109; TYRKINASE;

ProDom; PD000001; Euk pkinase; 1.

SMART; SM00219; TYRKC; 1.

SMART; SM00219; TYRKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1

PROSITE; PS001019; PROTEIN KINASE TYR; 1

PROSITE; PS0011; PROTEIN KINASE DOM; 1

Transferase; Tyrosine-protein kinase; A:
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DOMAIN 13

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SEQUENCE 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M Crittenden L.B., Raines M.A., Kung H.-J.; "C-erbB activation in ALV-induced erythroblastosis: processing and promoter insertion result in expressi amino-truncated EGF receptor."; Cell 41:719-726(1985).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=85228222; PubMed=2988784;
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InterPro; IPR001245; Tyr
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MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS IN SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
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MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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                                                  NGSKTPSIAAGVVGGLLCLVVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTPSGE 117
                                                                                                                                                            CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
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165
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634 AA;
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165
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52.3%; Pred. No. 7.66
tive 79; Mismatches
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ATP (BY SIMILARITY).

BY SIMILARITY.
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7.6e-87;
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                                        SEQUENCE OF 1-152 FROM N.A.

MEDLINE=84223957; PubMed=6328658;

Debuire B., Henry C., Benaissa M., Bi
Saule S., Martin P., Stehelin D.;

"Sequencing the erab gene of avian er

new type of oncogene.";

Science 224:1456-1459(1984).

-!- CATALYTIC ACTIVITY: ATP + a prote
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P00535;
21-JUL-1986
21-JUL-1986
15-JUN-2002
                                                                                                                              gene
Cell
[2]
                                                                                                                                                         MEDLINE=84026539; PubMed=6313229;
Yamamoto T., Nishida T., Miyajima N., Kawai S.,
"The erbB gene of avian erythroblastosis virus
                                                                                                                                                                                                                   Avian erythroblastosis virus (strain ES.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=79885;
                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein
   tyrosine phosphate.
-i-DISEASE: THE V-ERBB ONCOGENE ERYTHROBLASTS IN CULTURE AND IN CHICKENS.
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR000719; Fuk pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001019; PROTEIN KINASE DOM; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Tyrosine-protein kinase; AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K02006; AAA42394.1; ALT_INIT.
EMBL; K01216; AAA42400.1; -.
PIR; A00644; TVYUH.
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-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P11362; 1FGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 52.;
60; Conservative
                                                                                                         CAHFIDGPHCVKACPAGVLGENDTL-VRKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                                     YRSLLEDDDMGDLVDABEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                                                                                                                                                                                          IKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPP
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY)
BY SIMILARITY
BY SIMILARITY
R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
W; 76EBCDD06745D609 C
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Pred. No. 2.2e-84;
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                              Query Match
Best Local Similarity
Matches 341; Conserv
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SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS50011; PROTEIN KINASE PROFICE PS50011; PROTEIN KINASE, STROSTRE; PS051ne-protein kinase;
Glycoprotein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87064458; PubMed=2878364;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile
phenotype to ts167 avian erythroblastosis virus-transformed erythro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVIEU
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                             entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate.
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian erythroblastosis virus (strain ts167)
Viruses; Retroid viruses; Retroviridae; Avi
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P11273;
                                                                              SEQUENCE
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BIND
                                                                                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no rearriby non-profit institute.
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CATALYTIC ACTIVITY: ATP + a pro
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                                   69;
                                Score 1630; DB 1;
Pred. No. 1.6e-80;
9; Mismatches 119
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BY SIMILARITY.
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15-JUN-2002
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Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkles
Ullrich A., Vennstrom B., Schleßsinger J., Givol D.;
"Chicken epidermal growth factor (EGF) receptor: cDNA cexpression in mouse cells, and differential binding of transforming growth factor alpha.";
Mol. Cell. Biol. 8:1970-1978(1988).

-i- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDIN VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP
                                                                                                                                                                                                                                                                                        MEDLINE=88261272; PubMed=3260329;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
     SUBCELLULAR LOCATI
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900 (Rel. 13, Last sequence update)
02 (Rel. 41, Last annotation update)
growth factor receptor precursor (E
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Veognathae; Galliformes; Phasianidae; Phasiani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL. PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL. PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                al Similarity
310; Conserv
8 RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
IPR001245; Tyr pkinase.
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in kinase; ATP-binding; E
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%; Pred. No. 1.9e-78;
113; Mismatches 256; Indels
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POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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                LTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
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                                                                                                                                                                                                            AWPDNATDLYAFENLEI IRGRTKQHGQYSLAVVNLKIQSLGLRSLKEI SDGDI A IMKNKN
                                                                                                                                                                                                                                                                                        RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYIS
                                                                                                                                                                                                                                                                                                                                                                      DCCHNQCAAGCTGPRESDCLACRKFRDDATCKDTCPPLVLYNPTTYQMDVNPEGKYSFGA
                                                                          KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
                                                                                                     FSRQKECVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAHF
                                                 JCHPNCTRGCKGPGLEGCP---NGSK
                        708
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Search completed: July 22, Job time: 20.2793 secs 2003, 08:44:34

SEQ4-5-25-12 Entered (jdelaval 22-Jul-03 6:11)

GRYTFGASCUTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARWCYGLGMEHLREVRAV
TSANLOBFAGCKKIFGSLAFLPESFOODPASNTAPLQPEQLQVFETLEBITGYLY ISAMPDSLEDLSVFQ
NLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNTHLCFVHTVPMQQLFRNEPHQALLHT
ANREDBCCVESGLACHQLCARCHCWGPGPTQCVNCSQFLRGQECVESCRVLQGLFREYVNARHCLLPCHPE
CQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVD
LDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQCNIRKYTMRRLLQETELVEPLTPSGAM
PNQAQMRILKETELRKWCVLGSGAFGTVYKGINIPDGBLYKIPVAIKVTLRENTSPKANKEILDEAYVMAG
VGSPYVSRLLGICLTSTVQLVTQLMPYGCTLDHYRENRGRLGSQDLLNNCMQIAKGMSYLEDVRLVHRDL
ARNULVKSPHHYKITDFGLABLLDIDETEYHADGGKVPIKMALESILRRFTHQSDVMSYGVTVWELM
TFGAKPYDGIPAREIPDLEKGERLPQPPICTIDYMMIWKCMWIDSECRPFFRELVSEFSRMARDPGRF
VVIQNEDLGPARSPLASFLLEDDDMGDLVDAEEYLVPQGGFFCPDPAFGAGMVHHRHRSSSTRSGG
GDLTLGLEPSEEEAPRSPLAFSEGAGSDVFDGDLGMGAAKGLSSLFTHDPSPLQRYSEDPTVPLPSETDG
TVAPLTCSPQPEYVNQPDVRFQOPPSPREGPLPAARFAGAAKGLSSLFTHDPSPLQRYSEDPTVPLPSETDG
TVAPLTCSPQPEYVNQPDVRFQOPPSPREGPLPAARFAGATLERAKTLSPGKNGVKXVFAFFGGAVENPBY
TTOGGAARDHEBBNSFSAFNNI VYNDCONDBREGGASTGCTETSTANDEVLCI VYNDVI MELAALCRWGLLLALLPPGAASTQVCTGYİKANSKÉİĞİT EİLYQGCQVVQGNLELTYLPTNASLSFLQD IQEVQGYVLI AHNQVRQVPLQRLRIVRGTQLFENYALAYLDMGDPLNNTTPVTGASPGGLRELQLRSIT EILKGGVLİQRNPQLCYQDTILMKDİFHKNQULALTLIDTNRSRACHESSPMCKGSRCWGESSEDCQSLT RTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGİCELHCPALVTYNTDTFESMPNPE LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

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1.11.

Entered [jdelaval 22-Jul-03 6:21]

THSCVDLDDKGCPAEQRASPLTS IVSAVVGILLVVVLGVVFGILIKRRQOKIRKYTMRRLLOETELVEPL
TPSGAMPNQAQMRILKETELRKVKLUGGGAFTVKGIR DGENVKIP VAI KWILENTS KAANKEILDE
AYVMAGVGSPYVSRLLGICITSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLIMVQLAKQMSYLEDVR
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMALESIILRRFTHQSDVMSYGV
TVMELMTFGAKPYDGIPAREIDDLEKGERDDLDFTEYHADGGKVPIKMALESIILRRFTHQSDVMSYGV
TVMELMTFGAKPYDGIPAREIDDLEKGERDDAPPICTIDVYMINVKCWMIDSECRPFRBLVSEFSRMA
RDPQRFVVIQNEDLGFASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAFAGAGMVHHRHRSS
STRSGGGDLTIGLEBSEFEAPRSPLABSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL SEQ4-59-73-12

MELAALCRWGLLLALLÞPGAASTQVCTGTDMKLRLÞASÞETHLDMLRHLYQGCQVVQGNLELTYLÞTNAS
LSFLQDIQEVQGYÍKANSKÍ 191 t.elQRLRI VRGTQLFEDNYALAVLDNGDÞLNNTTÞVTGASÞGGLREL
QLRSLTEILKGGVL1QRNÞQLCYQDTILWKDIFHKNNQLAUTLLDTNRSBACHÞCSÞMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGÞLÞTDCCHEQCAAGCTGÞKHSDCLACLHFNHSGICELHCÞALVTYNTDTFE
SMPNÞEGRYTFGASCYTACÞYNYLSTDVGSCTLVCÞLHNQEVTAEDGTQRCEKCSKÞCARVCYGLGMEHL DLSVFONLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPH QALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHC LPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINC PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1 REVRAVTSANIQEFAGCKKI FGSLAFL PESFDGDPASNTAPLQPEQLQVFETLEEI TGYLYI SAWPDSLP

; Entered [jdelaval 22-Jul-03 6:21]

SRQ4-59-73-14

MELAALCRWGLLLALLPBGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
MELAALCRWGLLLALLPBGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIJGEVQfinif tvsfwlryshvsashleQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPYTGASP
GGLRELQLRSLTEILKGGVLIQENPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRC
WGESSEDQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPCHSDCLACLHFNHSGICELHCCALVTY
NTDTFESENPNPBERTYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTOQCCEKCSPCARVCYG
LGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA
WEDSLPDLSVFQNLQVIRGRIILHGAYSITLQGGIGISWLGRSLRELGSGLALLHHNTHLCFVHTVPWDQ
LFRNPHQALLHTANRFBDECVEGGLAACHQCLAGGIGVGGTGSTCAGGCTVEDCTLGETTGYLYISA
WEDSLPDLSVFQNLQVIRGRIILHGAYSITLQGGIGSWLGRSLRELGSGLALLHNTHLCFVHTVPWDQ
LFRNPHQALLHTANRFBDECVEGGLAACHQCLAGGIGVGGFTCVARCPSGVKPDLSYMPIWKFPDEGACQ
PCPINCTHSCVDLDDKGCPAEGRASPLTSIVSANVGILLVVUJLGVVFGILIKRRQKIKFVTMRRLLQET
ELVEPLTPSGAMPNQAQMRIILKETELRKVXLJGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKAN
KEILDEATVVMAGYGSPVYSRLLGICLTSTVQLVTQLMFYGCLLDHYRENFGRLGSQDLLNXCMMJ LSSILRRFTHQSD
VKSILDVARLVHRDLAARNVLVKSPNHVKITDFGLARLDIDETSYHADGGKVFIKMMALESILRRFTHQSD
VKSYGVTVWSLMTFGAKFYDGIPAFEIFTGGLARLDIDETSYHADGGKVFIKMMLESILRRFTHQSD
VKSYGVTVWSLMTFGAKFYDGIPAFEIFTGGLARLDIDETSYHADGGKVFIKMMLESILRRFTHQSD
VKSYGVTVWSLMTFGAKFYDGIPAFEIFTGSEAERTYBLLDDDMGDLVDAETSYLVGCSFFCPBAFCAGMVH
HRHRSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSE
BETWALDENSYLTDGCAANDDHDEDBEFSDEFSDEFDGAABGATLERAKTLSPGKNGVVKDV
KNUT FAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP V1

; Entered (jdelaval 22-Jul-03 6:37)
SEQ4-103-117-12
MELAALCRWGLLLALLPPGAASTOVCTGTDMKLRL

MELAALCRWGLILALLPBGAASTOVCTGTDMKLRLPASSETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRI VRCTQLFEDNYALAVLDNGDBLNNGY İ kanské i gi tel
QLRSLTEILKGGVLIQRNPQLCYQDTI ILWKDI FHKNNQLALTLI DTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGI CELHCPALTYNYTDTFE
SMPNPEGRYTFGAASCVTACPYNYLSTDVGSCTLVCPLHNQSCVLHFNHSGI CELHCPALTYNYTDTFE
SMPNPEGRYTFGAASCVTACPYNYLSTDVGSCTLVCPLHNQSCVALFBNHSGI CELHCPALTYNYTDTFE
SMPNPEGRYTFGAASCVTACPYNYLSTDVGSCTLVCPLHNQSCVAEDGTORCEKCSKPCARVCYGLGMBHL
REVRAVTSANIQEFAGCKXI FGSLAFILPESFDGDPATNAPLOPEQLQVFETILEEITGYLY I SAWPDSLIP
DLSVFQNLQVI RGRILHHGAY SLITLQGIGI SWLGLISLELGSGLALIHHNTHLCFVHTYPWDQLFRNNPH
QALLHTANR PEDECVGEGLACHOLCARCHCWGBGPTQCVVACOPEQLQVFETILEEITGYLY I SAWPDSLIP
DLSVFQNLQVI RGRILHHGAY SLITLQGIGI SWLGLISLAKETGSGCLALIHHNTHLCFVHTYPWDQLFRNNPH
QALLHTANR PEDECVGEGLACHOLCARCHCWGBGPTQCVVACOPEGRUXGDLS YMPI MKFDDEGACQPCP I NC
THSCVDLDDKGCPAGRASPLTSI VSAVVGILLVVVLGVVFGILLKRRQCNI RKYTMRRLLQFTELVEPL
TPSGAMPNQAQMRI LKETTELRKVXVLGSGA FGTVYKGTMI PDGENVKI PVA I KVLRENTS PKANKE I LDE
AYVMAGVGSPYVSRLLGI CLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLMNCMQI AKGMSY LEDVR
LVHDLAARNUL VKS PNHVKI TID PGLARLLDI DETEYHADGGKVY I KWMALESI LIRRRE FTHQSDVWSYGV
TVMELMTFGAKPYDGI PARE I PDLLEKGERLPQPP I CTI DVYMIMVKCMMI DSECRPR FRELVSEFSRMA
RDPQR FVVI QNED LGFSEELARRSPLAFSESCAGSDVDTDGDILGMGAKKGLOSLPTHDSP PLQRY SEBDPTVPL
STRSGGGDLTLCLEPSEELARRSP LAPSESCAGSDVDTDGDILGMGAKKGLOSLPTHDSP PLQRY SEBDPTVPL
PSETDGYVAPLTGSP PRESPENGP PSREGPLPAARPAGATLERAKTLSPGKNGVVKD VFAFGGA
VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYMDDQDP PBRGAPPSTFKGTPTAENPEYLGLDVPVI

; Entered [jdelaval 22-Jul-03 6:39] SEQ4-103-117-14

SEQ4-103-117-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLMNfnnftvsfalrykv
sashleqlrsutteilkggyliqrnpqlcyqdtilmkdifhkniglaltildtnrsrachpcspckgsc
wagssedcqsltrtveilkggyliqrnpqlcyqdtilmkdifhkniglaltildtnrsrachpcspckgsc
wagssedcqsltrtveilkggyliqrnpqlcyqdtilmkdifhkniglaltildtnrsrachpcspckgrc
wagssedcqsltrtveilkgyrliqrnpqlcygdtilmkdifhknigliglaltyrigr
wtdtrsmynavtsaniqsfagckifpcsctivcplhngevtaedbgtqrcekcspcarcyg
lcmellrvarpoliqrigrachtlogelgisklelgslrelgglalltlebttgtlyiisa
wpdslpdlsvrqnlqvigratilmgaysltlcqcigiswlgrelggcalllhwthlcfyltypwdq
lfrnphqallhtanredbecvgeglachqllcarghchgelrslrelggcalllhwthicfylfypwdq
lfrnphqallhtanredbecvgeglachqllcarghchgrpfcyargsyrpilkrpokityrpwdq
lfrnphqallhtanredbecvgeglachqlcarghchgrpfcyargsyrpilkrpokityrfyrilgebesacq
pcpincthscypysglicitlkykyllggartyrgjwpfglilkrrqokitkifvaritgrakgg
ylburlyhrdlaarnvlyksphykitdfglarllddeftyhadggkypikmhlesilrrrftqsb
wsygvtwelmtfgakrydgipareipblassearppgflctldwgakgloslpthdspraggmyh
hrhrssstrsggdltillergeryngpdvrspraggdlpaargakgloslpthdspragnykgu
pptyplsetdgyvapltcspqpeyyngpdvrpgsragglpaarpagatleraktilspgkngvykdv
pafggavenpeyltfogggaapqpphppafsparfdnlppragappstfkgddvykdv
pafggavenpeyltfogggaapqpphppafsparfdnlppragappstfkgddvykdv

; Entered [jdelaval 22-Jul-03 6:41]
SEQ4-149-163-12
MELAALCRWGLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQD1QEVQGYVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNYTTPVTGASPGGLREL
QLRSLTEILKGGVVLJAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDFLNYTTPVTGASCMGESSE
DCQSLTRTVCGAGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTNYTDTFE
SMPNPEGRYTFGASCVTA.CPANYLSTDVGSCTLVCPLHNQBVTAABGTQRCEKCSKPCGARVCYGLGMEHL
REVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAMPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISMLGLRSLRELGSGLALIHNUTHLCFVHTVPMDQLFRNPH
QALLHTAARPEDBCVGEGLAFCHQLCARGHCWGPGPTQCVNCSQFLRGGECVECCVLQCILREYVNARHC
LPCHPECQPQNGSVTCFGPEADQCVACAHYKDPFFCVARCPSGVTXDLSYMPIMKFPDEEGACQPCPINC
THSCVDLDDKGCPAEQRASPLTSIVSANVGILLVVVLGVVFGILIKRRQGKVTRRLLLGETELVEPL
TPSGAMENQAQMRILKETTELKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSSKANKEILDE
AYVMAGYGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLMWCMQLAKGMSYLEDVR
TVWELMTFGAKPVGGIPAREIDDLEKGERLPQPPICTIDVYMTMVKCMMIDSECRPFREELVSEFSRMA
RDPQRFYVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAGEFCDPPAPGAGGMVHHRHRSS
RTDSGCGLTGTE BESTEFE BBSELABESGLASSNAGELLAMACTIGGE DEVLEREN BY GENERALLES STRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

DPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPSPREGPLFAARPAGTTLERAKTLSPKKGVVKDV PAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP V1

; Entered [jdelaval 22-Jul-03 6:47]

SEQ4-210-224-12

MELAALCRWGLLLALIPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYGGCQVVQGNLELTYLPTNAS
LSFLQDIQEVGGSYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
LOLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPGYİKANBKİĞİLERİKSDCLACLHFNHSGICELKCPALVTYNTDTFE
SMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL
REVRAVTSANIQFFAGCKIFKYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHL
REVRAVTSANIQFFAGCKIFKIFGSLAFLPESFDGDDASNTAFLQFGOLQVFETLEEITQYLYISAWPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLCLRSLRELGSGLALIHHNTHLCFVHTVPNQDLFRNPH
QALLHTANRFEDECVGEGLACHQLCARGHCWGPGFTQCVNCSQFLRGQECVEECRVLQGLPREVVNARHC
LPCHPECQPQNGSVTCFGFEADQCVACAHYKDDPFCVARCPSGVKPDLSYNPIWKFPDEEGACQPCPINC
THSCUDLDDKGCPAEGRASPLTSIVSAVUGILLVVLGUVFGILIKRRQKIRKYTMRRLLQETELVEPL
TPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVALKVTREBTSPSKAMKEILDE
AYVMAGYGSPYVSRLLGICTSTYQLVTQLMPYGCLLDHVRENGRGLGSQDLLNWCMGIAKGMSYLEDVR
TVWELMTFGAKFYNGIPAREIPDLLEKGERLPQPPTCTIDVYMIMVXCWMIDSECRPRFRELVSEFSRNA
RDPRRFVIQNEDLGPASPLDSTFYRSLLEDDDWBGDLVDAEEXTLPQOGFFCPDPAPAGAGGWHTHRHRSS
STRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL
PSETDGYVAPLTCSPQFFSYNAPODPORPSPREGELDAARPAGATLERAKTLSPGKNGVKDVKDVFAFGGA
VENNEWYTTSCACAA NOOHDDBASCAA FROILLPAARPAGATLERAKTLSPGKNGVKDVKDVFAFGGA
VENNEWYTTSCACAA NOOHDDBASCAA FROILLPAARPAGATLERAKTLSPGKNGVKDVKDVFAFGGA
VENNEWYTTSCACAA NOOHDDBASCAA FROILLPAARPAGATLERAKTLSPGKNGVKDVKDVFAFGGA
VENNEWYTTSCACAA NOOHDDBASCAA FROILLPAARPAGAFTLERAKTLSPGKNGVKDLANDAACHAGATLANDAA

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SEQ4-210-224-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
MSTAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLLDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPfnnftv8fwlrvpkv8a8hleKHSDCLACLHFNHSGICELHCPALVTY
NTDTEESMPNPEGRYIFGASCYTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYG

; Entered (jdelaval 22-Jul-03 6:51) SEQ4-250-264-12

MELALICEMGLILALLP PGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEITYLPTNAS
LSFLQDIQEVQCYVLIAHNQVRQVPLQRLRI VRCTQLFENYALAVLDNGDPLNNTTPVTGASPGGLREI
QLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTYVCAGGCARCKSPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVQYIARINSK
£19itelRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQDGTORCEKCSKPCARVCYGLGMEHL
REVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDDASNTAPLQPBCQVPETLEEITGYLYISAWFDSLP
DLSVFQNLQVIRGRILHHQAYSLTTLQGCLISWLGLRSLEREGGLALHHNTHLCFVHTYWDQQLFRNPH
QALLHTANRPEDDECVGEGLACHQLCAGHKNDPFFCVARCTSGVKKDLSYMPIWKFPDEEGACQPCPINC
LPCHPECQDQNGSVTCFGEBADCVACAHKNDPFCVARCTSGVKKDLSYMPIWKFPDEEGACQPCPINC
THSCVDLDDKGCFABAGRASPLTSIVSAVVGILLVVLGVVFGILKRRQDKIRKYTMRRLLQETELVEPL
TPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGBENVKIPVAIKVTLRENTSPKANKSILDE
AVWAGVGSPYUSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLVTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLMPYGCLLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLDAPGCLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLDAPGCCLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLDAPGCCLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLDAPGCCLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYUSRLLGICLTSTVQLTQLDAPGCCLDHYRENRGRLGSQDLLMWCMQIAKGMSYLEDVR
AVWAGVGSPYGCTOTTURGLARLLDIDETSTANDGKVCCMMIDSCCRPFRELVSETSRMA
RDPQRFVVIQNEDLGFBASBLDSTFYRSLLEDDDWGDLDABEYLVPQDGFFCPDAPGAGAMVHHRHRSS
RDPGGGTTTURGTANDGARAGAMSTHRRS STRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

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SEQ4-250-264-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQD1QSVQGYVLIAHQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHBQCAAGCTGPHSDCLACCHFFNHSGICELHCPALVfnnftvsf
LCRSLTRTVCAGGCARCKGPLPTDCCHBQCAAGCTGPHSDCLACCHFRHSGICELHCPALVfnnftvsf
COMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISA
WPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGTSSLASLESGSLALLHHNTHLCFVHTVPWDQ
LFRNPHOALLHTAMRFBDECYCBSCLAGHQCAAGHCWGBGPTQCYWCSQPLRQGCCVEESGTRVGGTPREV
VNARHCLPCHPECQPQNGSVTCFGFBADQCVACAHYKDPFCVARCPSGVKPDLSYMPIWKFPDEEGACQ
PCPINCTHSCVDLDDKGCPASQDRASPLTSIVSAVGILLVVLJGVVFGILIKRRQOKIRKYTMRRLLQET
ELVEPLTPSGAMPNQAQMFILKETELRKVKVLJGSGAFFGTVYKGI HIPGGENVKI PVAIKULRENTSFKAN
KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLMWCMQIAKGMN
KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCCMQIAKGMN
KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCCMQIAKGMN
KEILDEAYVMAGVGSPYVSRLLGICLTSTVGLARLDDIDETSYHADGGRVFIKMMALESILRRRCTHQSD
VMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYNIMVKCWMIDSCCRPRFRELVS
UMSTGVTVWELMTGGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYNIMVKCWMIDSCCRPRFRELVS
EFSRMARDPQRFVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEXYLVPQQGFFCCPDPAFGAGGMN
HHRRSSTRSGGGDLTLGLESEBEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLGSLPTHDPSPLQRCMVKDV
FAFGGAVENDEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
VARGGAVENDESYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
VI

; Entered [jdelaval 22-Jul-03 7:10] SEQ4-325-339-12

TPSGAMPNOAOMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIPVAIKVLRENTSPKANKEILDE AYVMAGVGSPTVSRLIGICLTSTVQLVTQLMPYGCLLDFRRIGGLGSDLLNWCMQIAKGMSYLEDVR LVHRDLAARNVLVKSENHVKITDFGLARLLDIDETEYHADGGKVPIKMALESILRREFTHOSDVWSYGV TVMFLMTFGAKPYDGIPAREI PDLLEKGERLPOPPICTIDVNIM MVKCHMIDSECR PRFRELVSEFSRMA RDPQRFVLONSEDSPTYPSLLENGERLDDDMGDLUDLAYMINVKCHMIDSECR PRFRELVSEFSRMA RDPQRFVLONSEDSFYPRSLASSETYRSLEDDDMGDLUDLGMGAAKGLOSLPTHOPSPLORYSEDDTVPL PSETGGGDLTLGLEBSSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHOPSPLORYSEDDTVPL PSETGGGDLTLGLEBSSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHOPSPLORYSEDDTVPL PSETGGGDLTCGLEBSSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLOSLPTHOPSPLORYSEDDTVPL PSETGGVALPLTCSPQEYNQPDVROPPSPREGPLPARSPLAPSGAGATLERAKTLSPGKNGVVKDVPAFGGA DLSVPQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNTHLCPVHTVPWDQLFRNPH QALLHTANR PEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQBCVEGCRVLQGLPREYYNARHC LPCHPECQPQMGSVTCGFGPADQCVACAHYKDPFCVARCPSGVKPDLSXMPIWKFPDERGACQCFQINC THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPL DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFE SMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMgyi kanskfigitelefagcKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE

SMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMfnn
ft vsf wl tvpkvasahleepagckki roslafidesproddasktaepiggeolovytetleeitgylyisa
wpdsleplsyropolovie roslafidesproddasktaepiggeolalihunthilcfutpyldisa
wpdsleplsyropolovie roslafidesproddaskitesproddasktaeliggeolalihunthilcfutpyldid
LFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREY
VNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKLDVPLGVRACPSGVKPDLSYMPIWKFPDEEGACQ
PCPINCTHSCYULDDKGCPAEQRASPLTSIVSAAVVGILLVVLGVVFGILIKRRQXIKXYTMRRLLQET
ELVEPLTPSGAMPNQAQWRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKAN
KEILDEAVVMAGVGSPYVSRLLGICLTSTVQLVTQLWPYGCLLDVRENRGRCGSQDLLMWCNQJAKGMS
YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLDLDIFTEYHADGGKVPIKMMALESILRRRFTHQSD
VMSYGVTVWELMTFGAKKYDGIPAREIPDLLEKGERLPQPPICTIDVYNIMVKCMMIDSECRPRERELVS
ERSRMARDPQREVVIQNEDLGPASPLDSTFYRBLLEDDDMGLLVDAEEKILVPQQGFFCPDPAPGAGGMYH
HBHBGSGTBGCGGDLTIGLEBEEFARDES IL ABSEGNACENTENTENTYN TOTTUTE GENERGERUS ; Entered [jdelaval 22-Jul-03 7:10]
SEQ4-325-339-14
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLPEDNYALAVLDNGDPLMNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLLDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLFTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFE HRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSE DPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDV FAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVP

; Entered [jdelaval 22-Jul-03 7:14]

SEQ4-369-383-12

MELAALCREGLILALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQD1QEVQGYVLIAHQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDFLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGGARCKGFLFTDCCHEQCAAGCTGPHASDCTQRCEKCGSKPCARVCYNITDTFE
SMENPEGRYTFGASCVTACPYNLISTDVGSCTLVCPLHNQEVTAEDGTQRCEKCGSKPCARVCYGLGMqyi
kanskfigitelfefagCKKIFGSLAFLPESFDGDPASNTAPqyikanskfigitelTGYLYISAWPDSLP
DLSVFQNLQVIRGRILHNQAYSLTLQGLGISWLGLRSLREIGSGLALIHNTHLCFVHTVPWDGLFRNPH
QALLHTANRPEDBCVGEGLACHQLCARGHCWGFGFTQCVNCSQFLRGQECVECCRVLQGLPREYVNARHC
LPCHPECQPQNGSVTCFGFEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPINKFDDESGACQPCPINC
THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVYFGILIKRRQQKIRKYTMRRLLQFTELDDR
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRFFTHQSDVMSYGV
TVWELMTFGAKPVGGIPAREIPDLEKGGELDPFOCTLDHVTRENRGTGSQDLLMCMQJAKKGMSYLEDDR
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMMALESILRRFFTHQSDVMSYGV
TVWELMTGGAKPVGGIPAREDIFDTLEKGGELDPFOCTLDHVTRENRGTGGSQDLTLRRFFTHQSDVMSYGV
STRSGGGDLTLGLEFSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDFTWPL
SSTTDGYVAPLTCSPQPEYVNQDDVRPQPEPSPREGPFDARGATLERAKTLSPGKNGVVKDVFAFGGA
VURNBEVLTFDCGAA AGONED BASEBARNILVSUNDDSEFGABARTLSPKKNDVVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:14]

SEQ4-369-383-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDJQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCOSLTRTYCAGGCARCKGPLFTDCCHEQCAAGCTGPRHSDCLAACLHFRNSGICELHCPALVTNYTDTFE
SWPNPEERRYTFGASCVTACPYNLTSTDVGSCTJLVCPLHNQEVTAADGTQRCEKCSKPCARVCYGLGMfnn
ftvsfwlrypkvsashleffaGCKKIFGSLAFLPESFDCDPASNTAPQY kannskfigle leltgrivly
MPDSLPDLSVFQNLQVIRGRILHNGAYSITLCGLGISWLGRSLRELGSGLALIHHNTHLCFVHTPVBWD
LFRNPHQALLHTANREDECVGEGLACHQLCARGHCWGPGFTQCVNCSQFLRGQECVEECRLQGLPREV
VNARHCLPCHPECQDQNGSVTCFGFEADQCVACCHYKNDPPFCVARCPSGVKPDLSYMPIWRFDEEGACQ
PCPINCTHSCVDLDDKGCPAEGBASPLTSIVSAVVGILLVVVLGVVFGILIKRQOKIRKYTMRRLLQET
ELVEPLTPSGAMPNQAQWRILKETELKKVKLVGSATTVYKGIW PDGENVKIFVAIKTYMRRLLQET
ELVEPLTPSGAMPNQAQWRILKETELKKVKLVGSATTVYKGIW PDGENVKIFVAIKTYMRRLCGODLLMWCMQJAKGMS
YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLDIDETEYHADGGKVPIKMMALESILRRFFTHQSD
VMSYGVTWMELWTSGAKFYDGIPAREIDDLKGGRLDDDGDLVMAGKWLDSCRFRFRELVS
EFSRMARDDQRFWYUJQNBDLGPASPLDSTYBRSLLEDDDMGDLVDAGSKALLGSLFTHDPSPLAGRGMVH
HRHRSSTRSGGGDLTLGLEPSEEAPRSPLAFSEGAGSDVFDGDLGMGAAKGLGSLFTHDPSPLAGRGMVH
HRHRSSTRSGGGDLTLGLEPSEEAPRSPLAFSEGAGSDVFDGDLGMGAAKGLGSLFTHDPSPLAGN
DETYVLESETDGYVADLTCSPGEEXPNSDEEGAGSDVFDGDLGMGAAKGLGSLFTHDPSPLAND
DETYVLESETDGYVADLTCSPGEEXPNSDEEGAGSDVFDGDLGMGAAKGLGSLFTHDPSPLAND
DETYVLESETDGYVADLTCSPGEEXPNSDEEGAGSDVFDGDLGMGAAKGLGSLFTHDPSPLAND
DETYVLESETDGYVADLTCSPGEEYNNODDRENGESDLFAGATLERAKTLSPGKNOVKDU FAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVF V1

; Entered [jdelaval 22-Jul-03 7:17]

SEQ4-465-479-12

MELAALCRWGLILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
MELAALCRWGLILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDFLNNTTPVTGASPGGLREL
QLRSLTETLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLLDTNRRBACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLALTHLDTNRRBACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLALTHNTHLCFVHTVNTDTFFE
SMPNEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTORCEKCSKCCARCYCYGLMQYI
kanskfigitelEFGAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLQCLGISWLGARSLREGGGCALIHNTHLCFVHTVWBDQLFRQYI
KANSKfigitelECVGECLACHQLCARGHCWGPGPTQCVNCSQFLRGQGCCECRULQCLPRETYNARHC
LPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINC
THSCVDLDDKGCCPAEQRASPLTSIVSAVWGILLVVVLGVVFGILIKRRQGXCVTECRVLAGHETLDE
AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENGRLGSQDLLNWCMQIAKMSYLEDVR
LVHRDLARRNVLVKSGNIKTTDSCLARLLDIDTTSYHADGGKVPIKMALESILRRRFTHQSDVWSYGV
TVWELMFFGGAKPYDGIPAREIDDLLEKGERLPQPPICTIDVYMINVCMMIDSBCRPFRELVSEFSRMA
RDPQRFVVIQNEDGPASPLAFSEGAGSSDVFDGDLGMGAAKGLOSLFTHDPSPLORYSEDPTVPL
PSGAMPTOTIOLEPSEEBAPRSPLAPSEGAGSSDVFDGDLGMGAAKGLOSLFTHDPSPLORYSEDPTVPL
PSGAMPTOTIOLEPSEEBAPRSPLAPSEGAGSSDVFDGDLGMGAAKGLOSLFTHDPSPLORYSEDPTVPL
PSGAMPTONDDVEDGDDSDESDEBEEDI BAABBACATTERAUTT ERGCNAUTHVENER PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:17]

SEQ4 4465-479-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVBGTQLFEDNYALAVLDNGDPLNNYTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLFTDCCHBQCAAGCTGPKRSDCLACLHPRHSGICELHCPALVTYNTDTFE
SMPNPERGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHRQEVTAEDGTQRCEKGSKPCARVCYGLGMGY;
kanskfigitelefackvirlfgslaflpespdgdpasntaplqpedlqvfetleitgylyisawpdslp
blsvrqntqvirgrilhagaysltTLQGLGISWLGLRSLELGSGLALHHNTHLCFVHTVPWDQLFREn
ftvsfk wiltypkvsashleSCVGEGLAVCHQLARSHCHGSGPTQCVNCSQFLRGGECVECRVLQGLPREY
VNARHCLPCHECQPQNGSVTCFGPBADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQ
PCPINCTHSCVDLDDKGCPAEGRASPLTSIVSAVVGILLVVLGVVFGILIKRQQXIRKYTMRRLLQET
ELVEPLTSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVALKUMCMOIAKCMS
XELDVRLVHRDLAARNVLVKSPNHVKITDFGLARLDIDETSYHADGKVPIKMMALESILRRRFTHQSD
VWSYGVTVWBLMTFGAKPYDGIPAREIPDLEKGGELDDGDDGDLVAGESVLVCWMIDSECRPRFRELVS
EFSRNARDPQRFVVLONEDLGPASPLDSTFYRSLLEDDDMGDLVDAEESLLVPQQGFFCPDAPGAGGWYH
HRHRSSSTRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRVSE
DFTVPLPSSTTDGYVAPLTCSPPPEYVNQDVRPQPPSFREAGFLPAARFAGATLERAKTLSPEKNUVKDV
PARGCAVTUNDEVITTPCCCA ADDATED APGEBGADDT VANGANGATLERAKTLSPEKNUVKDV
PARGCAVATURDEVITTPCCCA ADDATED AFGEBGADDT VANGANGATLERAKTLSPEKNUVKDV
PARGCAVATURDEVITTPCCCA ADDATED AFGEBGADDT VANGANGATLERAKTLSPEKNUVKDV
PARGCAVATURDEVITTPCCCA ADDATED AFGEBGADDT VANGANGATLERAKTLSPEKNUVKDV
PARGCAVATURDEVITTPCCCA ADDATED AFGEBGADDT VANGANGATLERAKTLSPEKNUVKDV
PARGCAVATURDEVITTPCCCA ADDATED AFGEBGADDT VANGANGATLERAKTLSPEKNUVKDV FAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVP V1

; Entered [jdelaval 22-Jul-03 7:20]
SEQ4-579-593-12
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQD1GEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDFLNNTTPVTGASPGGLREL
QLRSLTEILKGGVVLIQRNPQLCYQDTILWKDIFHKNNOLALTLLDTNRSBACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTNYTDTFE
SKNNPEGRYTFGASCVTACFPNYLSTDVGSCTLVCPLHNQEVTAAEDGTQRCEKCSKCCARCYCYGLMQYI
KAANSKÍIGITELHCASVSLTLQGLGISMLGLRSLRELGSGLALIHNTHLCFVHTVPMDQLFRNPH
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISMLGLRSLRELGSGLALIHNTHLCFVHTVPMDQLFRNPH
QALLHTAKRPEDECVGEGLACHGLCARGKGWGPGPTQCVNCSQFLRAGQECVECRVLQGLPETNCH
LPCHPECQPQNGSYTCGGPADGCVACAHYKDDPFCVARCPGYIKANKIIJETLDE
THSCVDLDDKGCFAEGRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQGKVTECKVLRENTSSFANKEILDE
AVVMAGVGSPTVGRASPLTSIVSAVVGILLVVVFGILIKRRQGKVTESGALLHRRSTHQSDVRSYGV
TVMELMTGGAKPVGIPAEEIDLLEKGERLPQPFICTIDVYMINVCKWNIDSECRPFREELVSFFSRMA
RDPQRFVVIQNEDLGFAEFIDLLEKGERLPQPFICTIDVYMINVCKWNIDSECRPFREELVSFFSRMA
RDPQRFVVIQNEDLGFAEFILDSLLEKGERLPQPFICTIDVYMINVCKWNIDSECRPFREELVSFFSRMA
RDPQRFVVIQNEDLGFASPLDSTTYRSLLEDDDMGDLVDAGEFLVEFORDFGAGMWHRHRRS STRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:20]
SEQ4-579-593-14
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLHLLYGGCQVVQGNLELTYLPTNAS
LSFLQD1GEVQGYVLIAHNOVROVPLQRLRIVRGTQLFEDNYALAVLDNGDPLANTTPYTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQ5LTRTVCAGGCARCKGPLFTDCCHEOCAAGCTGPKHSDCLAACHFHNSGICELHCPALVTYNTDTFE
SWENPEGRYTFGASCVTAACPYNLSTDWGSCTLVCPLHNQEVTAABGTQRCEKCSKPCARVCYGLGMGY;
kanskfigitelefackvirgtruklstdvgcsctlvcplhngevtabedgrocekckskpcarvcygldmgy;
kanskfigitelefackkifgslaflpesfdgDpasntaplqpeQLQVFETLEEITGYLYISAWPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLREGSGLALIHNTHLCFVHTVPWDDQLFRNPH
QALHTAARPEDBCVGEGLACHQLCARGHCCWGPGPTQCVNCSQFTLRGGCCVECCRVLQGLPREYVNARHC
LPCHPECQPQNGSVTCFGGEADQCVACAHYKDPPFCVARCPfnnftvsfwlirRRQGLKRYTMRRLLQET
ELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKAN
KEILDEAYVMAGVSFYVSRLLGICLTSTVQLVTQLMFYGGLLDLYRENGRGLGSQDLLWCMQOIAKRGMS
YLEDVRLVHRDLAARNULVKSPNHVKITDFGLARLDIDETSYHADGGKVPIKMALESILRRFTHQSD
VMSYGVTVWELMTFGAKFYDGIPASPLDSTFYRSLLEDDDMGDLVDAEFKYLDNCKGMMYLDSSCRPRRELVS
ESSRMARDPQRFYVIQUBDLGPASPLDSTFYRSLLEDDDMGDLVDAEFKYLDNCKGMMYLDSPKTRDSPLGNYKS
ESSRMARDPQRFYVIQUBDLGPASPLDSTFYRSLLEDDDMGDLVDAEFKYLDSPLGNSPLORYSG
DFTVPLPSSTDGSYVAFLTGSPDSEEAPRSPLAFNIKTVADODDBEDAARSGANTLERKFTLDSPLORYSG
DFTVPLPSSTDGSYVAFLTGSPASPLDSTFYRSLLEDDDMGDLARAKFLSPGKNGVVKUV
FARGGAURDNEVITTGSPASPLDSTFYRSLLEDDDMGDLADARSKLDSSTLSPKKNGVKUV
FARGGAURDNEVITTGSPDDHPDBAFSABAFDATGABARGLASSENSTGATSRENGVGIVKDV
FARGGAURDNEVITTDGCAARDDDHPDBAFSABAFDATGABARGLASSENSTGATSRENGVGIVKDV
FARGGAURDNEVITTGDGCAARDDHPDBAFSABAFDATGABABGATLERAKTLSPGKNGVVKDV
FARGGAURDNEVITTGDGCAARDDHPDBAFSABAFDATGABABGATLERAKTLSPGKNGVVKDV FAFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVP V1

09-806703.pep

; Entered [jdelaval 22-Jul-03 7:26]
SEQ4-632-652-12

MELAALCRWGLLIAALLP PGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHFCSBMCKGSSRCWGESSE
QLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLIDTNRSRACHFCSBMCKGSSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLAGCLHFNHSGICELHCPALVTYNTDTFE
SMPNPEGRYTFGASCVVRCPYNYLSTDVGSCTLVCPLHNQBVTAEDGTQTCEKCSKPCARVCYGLGMQYİ
KANBKİİŞİLE 1EFAGCKKIFGSLAFLPESFDGDPASNTAPLQPBQLQVFETLEETTGYLYSAMPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLIRSLKELGSGLALIHNNTHLCFYHTVPWOQLFRRY
QALLHTANRPEDECVGEGLACHQLCARCHCWGFQPTQCVNCSQFLRGQECVEGCRILAGETREVXNAHC
LPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINC
THSCVULDDKGCFAEGRASPLTSIQFLYBIJFARAFAGAKVELDVRLVLBPLTPSGAM
PNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIFVAR KXTTWRKLLQETELVEFLTPSCAM
PNQAQMRILKETELRKVKVLGSGAFGTVYKGIMIPDGENVKIFVAR KYTWRRLLAGTTSFKAKELDEDAYVMAG
VGS PYVSRLLGICTTSTVQLVTQLMPYGCTLDHYRENRGRLGSQDLLNWCNQIAKGWSYLEDVRLVHRDI
ARNVLVKSPNHVKITDFGLARLDIDETEYHADGGKVPIKWALESILRRRFTHQSBVRSVCVTVWBLM
TFGAKFYDGIPAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDFQRF
VVIQNEDLGPAR PDLSTFYRSLLEDDDMGDLVDABESYLVPQGGFFCPDPAPGAGGMYHRHRHSSSTRSGG
GDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDFTVPLPSETDG
YVAPLTGSPQFEYNOQDDVRPQPPSPREGEPLAARAGATLERAKTLSPGKWGVVKDVFAFGGAVENPEY LTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:26]

SEQ4-632-652-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVGGYVLIANOVRQVPLQBLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
CLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAACCTGPRASDCTACLHFNHSGICELHCPALVTYNTDTFE
SMPNPEGRYTTGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMGY;
kanskijgitelefagckxifcgilftcgiswlglrslrelgggclalihnthlcfvhtvpwDQLfrnPh
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGGGCCVEECRVLQGLPREYVNARHC
LPCHEECQPOMGSVTCFGPEADQCVACALYXDPPFCVARCPGGVEDLSYMPIWRFDEEGACQPCINC
THSCVDLDDKGCPAEQRASPLTSIfnnftvsfwlrppFCVARCPGGVEDLSYMPIWRFDEEGACQPCINC
THSCVDLDDKGCPAEQRASPLTSIfnnftvsfwlrppFCVARCPGGVEDLSYMPIWRFDEEGACQPCINC
TPSGAMPNQAQMRILKETELRKVKVLGSGAFGTTVYKGTWIPDGERVKIFWAIKVLEENTSPKANKEILDE
AYWAGVGSPYVSRLLGICLTSTVQLVTCJMFYGCTLDHVRENRGRLGSQDLLNWCMGIAKGMSYLEDVR
LVHRDLAARNVLVKSPMHVKITDFGLAALLDIDETEYHADGGKVBIKMALESILRRFTHQSDVWSYGV
TVWELMTFGAKPYDGIPAREIPDLEKGERLPQPFICTIDVYMIMVKCCMMIDSECRPRFRELVSEFSRMA
RDPQRFVVIQDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAFGAGGWVHHRHRSS
STRSGGGDLTLGLEBSBEEARPSPLAPSEGAASBVFDGDDLGMGAAKGLGSLFTHDDSSPLQRYSEDFTYPL
PSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
VENPEYLTPQGGAAPQPHPPAFSPAFSDAFSDLYYMDQDPPERGAPPSTFKGTPTAENPEYLGLDVPVI

; Entered [jdelaval 22-Jul-03 7:29]

SEQ4-653-675-12

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRCTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKUNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSOCLACLHPNHSGICELKGPALVTYNTDTFE
SMPNPBERYTFGASCVTAKOPVNYLSTDUSGCTLVCPLHQUEVTAEDOTQRCEKCSKPCARVCYGLGMGYİ
kanskfigitelefackvifkgrlftpesfpdgpasntaplqeqlqvfetlelitgylyisawpbSLP
DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRRWH
QALLHTANRPEDECVGEGLACHQLCAGHYKDPFCVARCSGFLRGGGCVEECRVLQGLPREYVNARHC
LPCHPECQPQNGSVTCFGFEADQCVACAHYKDPPFCVARCSGVFLRGGECVEECRVLQGLPREYVNARHC
LPCHPECQPQNGSVTCFGFEADQCVACAHYKDPPFCVARCSGVFLRGDECVEECRVLQGLPREYVNARHC
LPCHPECQPQNGSVTCFGFEADQCVACAHYKDPPFCVARCSGVFBILIQYİANSKFİJEBAYVMAGVG
SYVSRLLGICLTSTVQLVTQLMFYGGILLVVLGVFGILLAWCMQJAKGMSYLEDVRLVHRADLAA
RNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRFTHQSDVSGVTVWELMTF
GAKPYDGIPAREIPDLLEKGERLDDDMGDLVDAEBYLVPQQGFFCPDPAFGAGMVHHRRSSSTRSGGAD
LTUGLEPSEEEAPRSPLAPSGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
APLTCSSQAFGTVNQDVRPGGLLVDLERAKTLSSGKMGVVXDVFAFGGAVENPEYLT
DCCCTA AB DCDUDDOSA FESD RENDIV VVANONDEFERA DDSCTFEXTENDER ANDENLOWAFGGAVENPEYLT
DCCCTA AB DCDUDDOSA FESD RENDIV VVANONDEFERA DDSCTFEXTENDER ANDENLOWAFGGAVENPEYLT
DCCCTA AB DCDUDDOSA FESD RENDIV VVANONDEFERA DDSCTFEXTENDER ANDENLOWAFGGAVENPEYLT
DCCCTA AB DCDUDDOSA FESD RENDIV VANONDEFERA DDSCTFEXTENDER ANDENLOWAFGGAVENPEYLT
DCCCTA AB DCDUDDOSA FESD RENDIV VANONDEFERA DDSCTFEXTENDER ANDENLOYLG LINUXI PQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVE NPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:33]

SEQ4-695-709-12

MELAALCRWGLLLALL PPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSELQDIQEVQGYVLIAHNQVRQVPLQRLRI VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLREL
QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTMRSRACHPCSEMCKGSRCWGESSE
DCQSLTRTVCAKGCARCKGPLPTDCCHEQCAGGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFE
SMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDDTQRCEKCSKPCARVCYGLGMQ/i
kanskiigitelefaGCKXIFGSILAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
DLSVFQNLQVIRGRILHNGAVSLTLQGLGISWLGLRSLRELGSGLALIHNTHLCFVHTVPNDQLFRNPH
QALLHTANRPEDECVGEGLACHQLCARGHCWGPGFTCVNCSQFLRGQECVEECRVLQGLPREYVNARHC
LPCHPEECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVEDLSYMPIWKFPDEEGACQPCINC
THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPL
TPSGAMPNQAQMRILKEGYİKANSKİGİLETITYKGIHYPDGENVKIPNAIKVLARNTSFKANKEILDE
AYWAGVGSPYVSRLLGICTITSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDUR
LVHRDLAARNVLVKSPNHVKITDFGLARLDIDETSYHADGGKVPIKMMALESILRRFFTHGSDVWSYGV
TVWELMTFGAKPYDGIPARFIPDLEKGERLPQPPICTIDVYMINVKCMMLDSECRPRFRELVSEFSRMA
RDPQRFVVIQNEDLGPASFLAPESGAGSDVFDGDLWBGAAKGLQSLBTHDBSPLQRXSEDFTYPL
PSGTDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGFDLARARPAGATLERAKTLSPGKNGVVKDVFAFGGA
VENPEYVIQCAAPOPHPPDAFSPAFDNLYYWGDDPPERGAPPSTFKGTFTAENPEYLGLDVPVI
PSETDGYVAPLTCSPQPEYNQPDVRPQPPSPREGFDLARARPAGATLERAKTLSPGKNGVVKDVFAFGGA
VENPEYVITPQCGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTFTAENPEYLGLDVPVI

; Entered [jdelaval 22-Jul-03 7:33]

SEQ4-695-709-14

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
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QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPRASDCLACLHFNHSGICELHCPALVTYNTDTFE
SMPNPEGRYTTGASCVTACPYNYLSTDVGSCTLVCPLHNOEVTABEDGTQRCEKCSKPCARVCYGLGMGY;
kanskfigitelffagcvkifrgslaftlesfdogdpasnynaplQpeglQVVESTLEEITGYLYISAWPDSLP
DLSVPQNLQVIRGRILHNGAVSLTLQGLGISNIGGLRSLRELGSGLALIHNTHLCFVHTVPWDQLFRNPH
QALLHTANRPEDECVGEGLACHQLCARCHCWGFGPTPCVNCSQFLRGQECVEECRVLQGLPREYVNARHC
LPCHPECQPDNGSVTCFGPEADQCVACAHYKDDPFCVARCPSGVRDLSYMPIWFPDEEGACQPCPINC
THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVVLGVVFGILIKRQQKIRKYTMRRLLQETELVEPL
TPSGAMPNQAQMRILKEfnnftvsfwlityNopefcVARCPSGVKDDLSYMPIWFPDEEGACQPCPINC
TPSGAMPNQAQMRILKEfnnftvsfwlityNGVTUFGYGLLDHVRENRGRLGSQDLLNWCMQIAKGMS
YLEDVRLVHRDLAARNVLVKSDMYVKITDFGLARLLDIDETEYHADGGKVVIKWALLESILRRFTHQSD
VMSYGVTVMELMTFGAKPYDGIPAREIPDLLEKCERLPOPPICTIDVYMIMVXCMMIDSECRRFRELVS
EFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMWH
HRHRSSSTRSGGGDLTIGLEBSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKAGLQSLFTHDSPSLQRYSE
DFTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPSPREGPLPAARAGLASILERAKTLSPGKNGVVKDV
FAFGGAVENPSYLTPQGGAAPQPPPPAFSPAFDNLYYNDQDPPERGAPPSTFKGTPTAENPEYLGLDVP
V1

; Entered [jdelaval 22-Jul-03 7:35]

SEQ4-710-730-12

MELAALCRWOLLIALLEPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
LSFLQD1QEVQGYVL1AHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASSGGLREL
QLRSLTEILKGGVL1QRNPQLCYQDT1LWKD1FHKNNQLALTL1DTNRSRACHFGSFMCKGSSCMGESSE
DCQSLTRTVCAGGCARCKGFLPTDCCHEQCAAGCTGFKHSDCLACLHFNHSG1CELHCPALVTYNTDTFE
SMPAPEGRYTTGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCCKCSKFCARVCYGLGMGY1
KANBKfigitelEFACCKK1FGSLAFLPESFDCDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
DLSVFQNLQVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHNTHLCFVHTVPMDQLFRNPH
QALLHTANRPEDECVGEGLACHQLCARCHCWGPCPTQCVNCSQFLAGGCCVEECRVLQGLPRSYVNARHC
LPCHPECQPONGSVTCFGFPADQCVACAHYKDPPFCVARCPSGVKPDLSYNPIWKFPDEEGACQPCPINC
THSCVDLDDKGCPAEQRASPLTSIVSAVVGILLVVLGSVFFGLLIKRRYTMRRLLQETELVEPL
TPSGAMPNQAQMRILKETELRKVKVLGSGAFGQYiKanskfigitelVLRENTSPKAAKEILDEAYVMAG
USSPYVSRLLGICTSTVQLVTQLMFYGCLLDHYRENGRAGSQDLLMWCWQIAKCMSYLEDVRLVHRDL
AARNUVLKSPNHVKITDFGLARLLDLDETYHADGGKVPIKMALESILRRRFTHQSDVMSYGVTVWELM
TFGAKPYDGITAREIPDLLEKCERLPQPPICTIDVYMIMVKCMMIDSECRPRFRELVSEFSRWARDPQRF
VIONEDLGPASPLDSTFYRSLLEDDDMGDLVDAEELVAPQOGFFCPDPAPGAGGMVHHRHSSSTRSGG
GDLTLIGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDG
YVAPLTCSPOPEYVNODDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKGVVKDFAFGGAVENPEY
LTPQGGAAPQPPPPPAFSPAFDNLYYMDQDPPPRRGAPESTFKGTFTAENPEYLGLDVPV1

; Entered [jdelaval 22-Jul-03 7:35]
SEQ4-710-730-14
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNAS
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QLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSE
DCQ5LTRTVGAGGCARCKGPLFTDCCHEQCAAGCTGPKBSDCLACCHFRHSGICELHCPALVTWTDTFF
SMPNPEGERYTFGASCVTACPYXVLSTDVGSCTLVCPLHNQEVTAABGTGNCEKSKPCARVCYGLGMGY;
kanskfigitelferaccvxicfschlorgcrfcchecgschluchthrithcfvhftpvpwDGLFRNPH
QALLHTANRPEDECVGEGLACHQLCARGHCWGPGFTQCVNCSQFLRGQECVECCRVLQGLPREYVNARHC
LPCHBECQPQNGSVTCFGTEADQCVACAHYKDPFFCVARCPSGVKPDLSYMPIKFPDDEGACQDCPINC
LPCHBECQPQNGSVTCFGTEADQCVACAHYKDPFFCVARCPSGVKPDLSYMPIKFPDDEGACQDCPINC
THSCVDLDDKGCPASQRASPLTSIVSAVVGILLVVVLGVVFGILIKRQQXIRKYTMRRLLQTTELVEPL
TTSGAMPNQAQMRILKETELRKVXVLGSGARGINftvsfinftvsfilrknogXilkmcMQJAKKGMSYLEDWR
LVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGKVPIKMMALESILRRFTHQSDVMSYGV
TVMELMTGGAKPYGGI PAREIPDLEKGGRLADLDDGTCYMTMVKCMMIDSECRPRFELVSSFSRMA
RDPGRFTVIQNEDLGASPLSTFYRSLLEDDDMGDLVDAESYLVDQGGFFCDBAPGAGRWHRHRRS
STRSGGGDLTLGLEPSEEAPRSPLAPSEGAGSDVPDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPL
PSGTADGYVAPLTCCSPPEYYNQDPDRFQPPSFREGPLLABSYLARGKNISPEGKGVVKDVFAFGGA
LUNDETUTDGCGA ADDRESCARDERGANDESCARDCTGCTGARANDESULVERD

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GENERAL IMPORMATION:
APPLICANT: Sceinaa, Lucilla
APPLICANT: Mouriteen, Soren
APPLICANT: Mouriteen, Soren
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APPLICANT: Leach, Dana
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GENERAL INFORMATION:
APPLICANT: Steinas, Lucilla
APPLICANT: Mouritsen, Soren
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APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Dalum, Iben
APPLICANT: Leach, Dana
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus
APPLICANT: Nielsen, Klaus
APPLICANT: Rasmussen, Gunilla
APPLICANT: Rasmussen, Peter
ITILE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT FILING DATE: 19301-04-04
PRIOR APPLICATION NUMBER: US/09/806,703A
CURRENT FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR APPLICATION NUMBER: DK 1998 01261
PRIOR APPLICATION NUMBER: US 60/105,011
APPLICATION NUMBER: US 60/105,011
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 12
LENGTH: 15
TYPE: PRT
ORGANISM: Clostridium tetani
US-09-806-703A-12
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steinaa, Lucilla
APPLICANT: Mouritsen, Soren
APPLICANT: Mouritsen, Soren
APPLICANT: Mouritsen, Soren
APPLICANT: Mouritsen, Soren
APPLICANT: Haaning, Jesper
APPLICANT: Haaning, Jesper
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus
APPLICANT: Karlsson, Gunilla
APPLICANT: Karlsson, Gunilla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3531-0109P
CURRENT APPLICATION NUMBER: US/09/806,703A
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/DK99/00525
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 14
LENGTH: 21
TYPE: PRT
US-09-806-703A-14
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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(c) 1993 - 2003 Compugen Ltd.
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Q85468
Q9WVF5
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Q9UK79
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Q9EP98
Q9YH40
Q9W6F6
P79754
                                                                                Q8R2X1
Q86712
                                                                                      O18735 canis famil
O399X70 rattus norv
O39998 mus musculu
O39464 xiphophorus
O394616 gallus gall
p79754 fugu rubrip
O394619 anopheles g
O39471 mus musculu
O86712 avian rous-
                                                                                                                                                                                                                                Description
                                                    Q86714 avian rous-
Q8wyv0 homo sapien
Q64895 avian eryth
                 Q85468 avian eryth
Q9wvf5 mus musculu
Q9erv6 mus musculu
                                        A yokota H.;

yokota H.;

"cDNA cloning of erbB-2 from canine mammary gland.";

"cDNA cloning of erbB-2 from canine mammary gland.";

"cDNA cloning of erbB-2 from canine mammary gland.";

REMEL, AB008451; BAA23127.1; -.

REMEL, AB008451; BAA23127.1; -.

REMEL, AB008451; BEA223127.1; -.

REMEL, AB008451; BEA223127.1; -.

REMEL, AB008451; BEA223127.1; -.

REMEL, AB008451; EGFR_L domain.

InterPro; IPR000494; EGFR_L domain.

RINterPro; IPR001245; Tyr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

RINterPro; IPR001245; Tyr_pkinase.

RINterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00059; Purin-like; 1.

DR Pfam; PF00059; Purin-like; 1.

DR Pfam; PF00059; pkinase; 1.

DR Pfam; PF00059; pkinase; 1.

DR Pfam; PF00059; pkinase; 1.

DR Pfam; PF00059; pkinase; 1.

DR Pfam; PF00059; pkinase; 1.

DR Pf000m; PD000001; Euk pkinase; 1.

DR Pf000m; PD000001; Euk pkinase; 1.

DR Pf000m; PD000001; PVKC; 1.

DR Pf000m; PD00001; PVKC; 1.

DR Pf000m; PD00001; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

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DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
NCBI TaxID=9615;
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01-JUN-2002 (TrEMBLrel
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Q14256
Q9923V5
P11776
Q8ZW1
Q99V62
Q99UD7
Q9HUD7
Q9HUD7
Q9HUD7
Q9HUD7
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Q9VD94
Q91YM0
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O90836 gallus gall
O90850 rattus norv
O90852 gallus gall
O14556 homo sapien
O923v5 rattus norv
P11776 xiphophorus
O882v1 droscophila
O99162 xiphophorus
O99162 xiphophorus
O99162 xiphophorus
O99107 homo sapien
O901v5 biomphalari
O901v5 biomphalari
O901v6 oryctolagus
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Q23821 caenorhabdi
Q26566 schistosoma
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073798 xenopus lae
073798 xenopus lae
09u5a8 bombyx mori
08uw84 paralichthy
08uw83 paralichthy
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Q96135 homo sapien
Q99mr2 mus musculu
Q07912 homo sapien
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Q9ygh8 scophthalmu
Q9qvw4 rattus sp.
Q9qvw4 rattus sp.
Q9vd94 drosophila
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093457 scophthalmu
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EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEG
                                 IDSECRPRFRELVSEFSRMARDPORFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDA 1020
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                                                                 HOSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLDOPPICTIDVYMIMVKCWM
                                                                                HQSDVMSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPBICTIDVYMIMVXCWM
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                     YVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIAKGMSYLEDVR
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Pred. No. 0
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REMBL; M37394; ARF14008.1; -

RESSP; P11362; 1FGK.

RINterPro; IPR000749; EGFR L domain.

RINterPro; IPR000719; Euk pkinase.

RInterPro; IPR0007174; Furin-like.

RInterPro; IPR001245; Tyr_pkinase.

RInterPro; IPR001245; Tyr_pkinase.

Pfam; PF00059; pkinase; 1.

R Pfam; PF01030; Recep_L domain; 2.

PR PRINTS; PR00109; TYRKINASE.

DR PRONTS; PR001001; FU; 3.

SMART; SM00261; FU; 3.

PR SMART; SM00219; TYRK; 1.

PR PROSITE; PS00117; PROTEIN KINASE DOM; 1.

PROSITE; PS00119; PROTEIN KINASE TYR; 1.

PROSITE; PS00119; PROTEIN KINASE TYR; 1.

PROSITE; PS00119; PROTEIN KINASE TYR; 1.

R PROSITE; PS00119; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

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                                                                                                                   Query Match
Best Local Similarity
Matches 642; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FISHER, TISSUE=LIVER, Guttridge K., Dawson T.L., Earp H.S., Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A truncated, secreted form of the epidermal grencoded by an alternatively spliced transcript Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QX70
Q9QX70;
01-MAY-2000
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Petch L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90558888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Earp H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Epidermal growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
3 LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1200
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                                                                                                                Conservative
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                                                                                                                                           46.6%;
                                                                                                             167;
                                                                                                 Score 3171; DB 11;
Pred. No. 2e-230;
7; Mismatches 354;
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                                                                                                                                  LVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSPLA 1076
                                                                                                                                                                                                                                                                     SSLSANSN---
                                                  PSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCS
                                                                                                                                                                                    CWMIDADSRPKFRELILEFSKWARDPORYLVIOGDERMHLPSPTDSNFYRALMEEEDMED
                                                                                                                                                                                                              CWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDDMGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP-LTSIVSAV
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Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recept_domain; 2.
PF10130; Recept_domain; 2.
PF10130; PR00109; TYRKINASE.
PF20Dom; PD000001; Buk_pkinase; 1.
PF20Dom; PM00201; TYRKINASE; 1.
SMART; SM00220; STKC; 1.
SMART; SM00219; TYFKC; 1.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00119; PROTEIN KINASE ATP; 1.
PROSITE; PS001019; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.
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O9EP98
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O1-MAR-2001 (TrEMBLrel. 16
O1-MAR-2001 (TrEMBLrel. 2)
O1-JUN-2002 (TrEMBLrel. 2)
                                                                                                                                                                                                                                                        EMBL; AF275366; AAG28045.1; -...EMBL; AF275366; AAG28045.1; JOINED. EMBL; AF275366; AAG28045.1; JOINED. EMBL; AF275367; AAG28045.1; JOINED. EMBL; AF275367; AAG284386.1; -...HSSP; P11362; IFGK.

MGD; MGI:95294; EGfr.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_bKinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001257. Tyr_pkinase.
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STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3Plus...
EGFR.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse alternative Egfr transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reiter J.L., Threadgill D.W., Eley G.D., St. Schehl C., Pearsall R.S., Green P.J., Yee D. Balasubramaniam S., Crossley T.O., Magnuson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative genomic sequence analysis and isolation of human mouse alternative Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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16, Last sequence update)
21, Last annotation update)
receptor isoform 1.
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Strunk K.E., Danielsen e D., Lampland A.L., son T.R., James C.D.,

A.J.,

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SEQUENCE 1210 AA; 134840
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Pred. No. 3.1e-228;
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InterPro; IPR000345; CytC heme bind.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000199; Euk pkīnase.
InterPro; IPR002174; Furin-like.
InterPro; IPR0012174; Furin-like.
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InterPro; IPR001245; Tyr pkinase.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF001030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PF000109; TYRKINASE.
ProDom; PF000109; TYFKC; 1.
SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00134; GRAM POS ANCHORING; UN PROSITE; PS00134; GRAM POS ANCHORING; UN PROSITE; PS00110; PROTEIN KINASE BATP; 1.
PROSITE; PS00110; PROTEIN KINASE TOR; 2.
PROSITE; PS00101; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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O9YH40; O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations."; Oncogene 16:1681-1690(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
Dimitrijevic N., Winkler C., Wellbrock
Altschmied J., Schartl M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xiphophorus xiphidium.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                             EMBL; U53471; AAD10500.2;
HSSP; P11362; 1FGK.
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Submitted (JUL-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor tyrosine XMRK.
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                                                                                         MAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGM
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                IMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPASPLDSTFVRSLLEDDD
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IILKCWMIDPSSRPRFRELVGEFSQMARDPSRYLVIQG---NLPSPSDRRLFSRLLSSDD
                                                                                                                                        MASVDHPHVCRLLGICLTSAVQLVTQLMPYGCLLDYVRQHQERICGQWLLNWCVQIAKGM
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  Query Match
Best Local Similarity
Matches 539; Conserv
                                                                                                                                                                        PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYPKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
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O9W6F6;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,

O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Distribution of neuregulin-1 (nrg1) and embryonic chick hindbrain.";
Mol. Cell. Neurosci. 13:258(1999).
EMBL; AF121963; AAD31764.1;
HSSP; P11362; IFGK.
                                                                                                          Kinase; Tyrosine-protein kinase.
NON TER 1 1
SEQUENCE 1137 AA; 127927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain;
Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001368; TNFR c6.
InterPro; IPR001245; Tyr kinase.
InterPro; IPR004019; YIP motif.
Pfam; PF00757; Furin-like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99263203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=HINDBRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                            40.1%;
                                                                                                       127927 MW;
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Score 2729.5;
Pred. No. 4.1e
69; Mismatches
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Last annotation updat
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                                                                                                          4D616436F87DC84F CRC64;
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                      9.5; DB 13;
4.1e-197;
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Conservative

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                                                                                                                                                                                            NRNQFVYRDGGYAAEQGV-PMPYRAPGCIIPEAPVAQGATAEIFEDTCCNGTLRKQVATL
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PHPPPAFSPAFDNLYYWDQDPPERGA--PPSTFKGTPT
                                                                                                                                      THDPSPLQRYSEDPTVPLPS------ETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREG
                                                                                                                                                                                                                                RHRSSSTRSGGGDLTLGLEPSEEEAPRS--PLAP-SEGAGSDVFDGDLGMGAAKGLQSLP
                                                                                                                                                                                                                                                                           LVIQGODRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVP-QAFNIPPPIYTSRTRIDS
                                                                                                                                                                                                                                                                                                                 VVIQNED-LGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHH
                                                                                                                                                                                                                                                                                                                                                          PTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRY
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                                     DLQAVDNPEYHN-----APNGQPKAEDEYVNEPLYLNTFANTLENAEYL-----K 1055
                                                                            PLPAA-RPAGATLERAKTLSPGKNGVVKDVF-----
                                                                                                                  AKEDSSTORYSADPTVF1PERV1RGELDEDGYMTPMRDKPKTDYLNPVEENPFVSRRKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ARLLEGDEKEYNADGGKMPIKWMALECIHYRKFTHQSDVWSYGVTIWELMTFGGKPYDGI</u>
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                                                                        -AFGGAVENPEYLTPQGGAAPQ 1206
AENPEYL 1249
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Matches 52
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Pfam; PF00069; pkinase; 1.
Pfam; PF000069; Recep L domain; 2.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00117; PROTEIN KINASE DOM; 1.
ATP-binding; Transferase.
SEQUENCE 1328 AA; 148613 MW; A333033
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P79754;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99177347; PubMed=10077531;
Gellner K., Brenner S.;
Gellner K., Brenner S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ErbB3.
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InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF056116; AAC34391.1; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 9:251-258(1999).
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524; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
IDSFINCTKIQGSLHFLVTGILGDDFKNVPPLDAKKLEVFRTVREITDILNIQSWPKELN
                                                                                                                                                                                                                                                                 AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY
                                                                                                                                                                                                                                                                                                                                                                      LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YPKDG--PSGLNQLGLMNLTEILDGGVQIINNKYLRYGPWVYWRDII-RNNDAPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
                                                                                                            HFV-VDGSSCVSVCPPDKMEV--ERGSQRQCELCSGLCPKVCEGTGAE---QRQTVDSSN
                                                                                                                                                             NYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                                                              AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPT
                                                                                                                                                                                                                                                                                                                                IQFNGERGVCH---KSC-GNYCWGPGKDQCQILTKTVCAPQCNDRCFGTSPRDCCHIECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WRLILMCVASRLRAASSOTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI
                                                      IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
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OC 1
Q9BIH9 PRELIMINARY; PRT; 1433 AA.
Q9BIH9;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment).
EGFR.
Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culi
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InterPro; IPR0022174; Furin-like.
InterPro; IPR00229; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00059; pkinase; 1.
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SEQUENCE FROM N.A.

Doherty J.K., Clinton G.M., Adelman J
Submitted (SEP-2000) to the EMBL/GenB.
SMBL; AF177761; AAD56009.2; -
EMBL; AF177761; AAD56009.2; -
InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-like.
Pfam; PF01030; Recep L_domain; 1.

Pfam; PF01030; Recep L_domain; 1.

SMART; SM00261; FU; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doherty J.K., Bond C., Jardim A., Adelman J.I "The HER-2/neu receptor tyrosine kinase gene autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=99415951; PubMed=10485918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Butheria; Rodentia; Sciurognathi;
                                                                                                                                                Q8R2X1
                                   NCBI_TaxID=10090;
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 Strausberg R.;
Submitted (APR-2002)
                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCARCKGPLPTDCCHEOC
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                                                                                                                                                                                                                                                   LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAP 387
                                                                                                                                                                                                                              IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQP 394
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   the EMBL/GenBank/DDBJ
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Pred. No. 3.6e-1
5; Mismatches
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EMBL/GenBank/DDBJ databases.
                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR000719; Buk pkinase.

InterPro; IPR000728; Retro M.

InterPro; IPR001245; Tyr pkinase.

InterPro; IPR001245; Tyr pkinase.

Pfam; PF02063; pkinase; 1.

ProDom; PD000001; Buk pkinase; 1.

R ProDom; PD000001; Buk pkinase; 1.

R SMAIT; SM00219; TyrKc; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

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Hypothetical
SEQUENCE 36
                                                                                                                                                                                                                                                                                 Vennstrom B., Raynoscheck C., Jansson L., Doe Johnsson A., Beug H.;
Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene evolution of distinct viral genomes carrying different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; 569372; AAC60725.1; -.
HSSP; P03322; 1A65.
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Q86712;
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MEDLINE=94203659; PubMed=8152791;
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Viruses; Retroid virus
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367 AA; 4
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ses; Retroviridae;
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11; Mismatches
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                                                                                                                               PTHDPSPLQRYSEDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPA
                                                                                                                                                                                      HRSSSTRSGGGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSL 1101
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                                                                                   ARPAGATLERAKTLSPGKNGVVKDVF-----AFGGAVENPEYL
                                                                                                                                                               -NSPST-----RNGQGH
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 PRELIMINARY;
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                                                             -TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL
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Pred. No. 3.9e-121;
75; Mismatches 118;
 PRT;
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Q86714;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
           Vennstrom B., Raynoscheck C., Jansson L., Doe Johnsson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene evolution of distinct viral genomes carrying different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; S69372; AACG0727.1; ...
HSSP, P11362; IFCK.
                                                                                                                                              NCBI_TaxID=11950;
                                                                                                                                                               Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                         V-ERBB.
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MEDLINE=94203659; PubMed=8152791;
  IPR000719;
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Euk_pkinase
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PRODOM; PD000001; EUK pkinase; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00107; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

Tyrosine-protein kinase.
                                                                           QBWYVO PRELIMINARY; PRT; 412 AA. QBWYVO; CHARR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation updat Hypothetical 44.7 kDa protein.
Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567 AA; 63390 MW;
                                                                                                                                                                                                                                                                                                                                                                   --TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL
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Chordata;
Primates;
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  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C6D9CBA7ADF725E1 CRC64;
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Best Local S
Matches 330
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Pfam; PF02757; YLP; 2.

ProDom; PF020001; Euk_pkinase; 1.

SMART; SM00219; TYTKC; 1.

PROSITE; PS00018; EF HAND; UNKNOWN 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Hypothetical protein.

SEQUENCE 412 AA; 44702 MW; 034397FF3
                                                                                                                                                            Q64895 PRELIMINARY; P
Q64895; O1-NOV-1996 (TrEMBLrel. 01, Cre
01-NOV-1996 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Gag, V-erb-A, V-erb-B protein.
GAG, V-ERB-A, V-ERB-B,
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retro
SEQUENCE FROM N.A.

MEDLINE=90206603; PubMed=1969616;

Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman
"Six amino acids from the retroviral gene gag greatly enhance
transforming potential of the oncogene v-erb-B.";
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Wan D.F., Gu J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002048; EF-hand.
InterPro; IPR000719; Ebk pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR0014019; YLP motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF318349; AAL55856.1;
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[1]
                                                                                                                                          NCBI_TaxID=11861;
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                                                                                                                                                                      Retroviridae;
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Last annotation updat
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Pred. No. 8.3e
5; Mismatches
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                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                PRT;
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8.3e-120;
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InterPro; IPR000719; Stdhrmn_receptor.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR00124; STROIDFINGER.

InterPro; IPR00124; STROIDFINGER.

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InterPro; IPR00125; InterPro; I.

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Best Local Similarity
Matches 358; Conser
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-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SUBLIARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                     1047
                                                                       822
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X52211; CAA36459.1; JOINED.
P10828; 2NLL.
                                                                                                                                                                                                            HRSSSTRSGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDP
                                                                                        VIQ-NEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR
                                                                                                                                     RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
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                                                                     VIOGDERMHLPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHOGFF
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Pred. No. 6.2e-116;
3; Mismatches 142;
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 SRTPLLSSLSATSN----
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Best Local Sim
Matches 345;
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Q85468;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000001; Euk pkinase; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50011; PROTEIN KINASE TYR; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

ATP-binding; Transferase; Tyrosine-protein kinase.

SEQUENCE 545 AA; 60899 MW; 140DCE8CCA0F8AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Common site of mutation in the erbB gene of avian erythroblastosis virus mutants that are temperature sensitive for transformation."; Oncogene Res. 1:65-278 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Ts34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X06943; CAA30024.1;
HSSP; P11362; 1FGK.
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KGERLPQPPICTIDVYMIMVKCWMSDADSRPKFRELIAEFSKWARDPPRYLVIQGDERWH
                                  KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
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54.9%; Pred. No. 1.2e
tive 70; Mismatches
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No. 1.2e-115;
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RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konnoh S., Yamanaka I.,

RA Arakawa T., Hara A., Fukunishi Y., Konoho S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;
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Q9WVF5;
01-NOV-1999
01-NOV-1999
01-JUN-2002
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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"Alternative Transcripts from the Human
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Mammalia; Eutheria;
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12, Last sequence update)
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receptor (Epidermal growth
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m S., Crossley T.
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Sciurognathi; Muridae;
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Nature 409:685-690(2001).
EMBL; AF124513, AAD44149 1; -
EMBL; AF275366; AAG28047.1; -
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EMBL; AF275365; AAG28047.1; JU
EMBL; AK004944; BAB23688.1; -
EMBL; AK004944; BAB23681.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                            LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQE
IMGENNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGC
                      VKPDLSYMPIWKFPDEEGACOPCPINCTHSCVDLDDKGC
                                               CNILEGEPREFVENSECIOCHPECLPOAMNITCTGRGPDNCIOCAHYIDGPHCVKTCPAG
                                                               CRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG
                                                                                                  KLEGTPNOKTKIMWNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDC
                                                                                                                         QLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEE
                                                                                                                                                  AFENLEIIRGRTKQHGQFSLAVVGLNITSLGLRSLKEISDGDVIISGNRNLCYANTINWK
                                                                                                                                                                         VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
                                                                                                                                                                                                     FKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDLH
                                                                                                                                                                                                                     FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
                                                                                                                                                                                                                                                       VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFKDTLSINATNIKH
                                                                                                                                                                                                                                                                                                                        CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                           -QSHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                                                                                                                                                                                                                                        DTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                            -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                           VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                                                                                                                                                                                                                                          CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN
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IPR002174;
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Pred. No. 4.1
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Mismatches 233;
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arch completed: July 22, 2003, 08:11:27 time : 133.375 secs

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Minimum DB
Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                      seq length: 0
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6842
1 MELAALCRWGLLLALLPPGA.....TFKGTPTAENPEYLGLDVPV 1261
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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pir2:
pir3:*
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SUMMARIES

Result No.	62 62	108	gt 25	DB DB	ID
. μ	6626	96.8	1255	, –	A24571
انا	584		1260	، بر	TVRTNU
4.	3118	45.6	1210	_	GQHUE
U	'n	45.1	1210	2	A53183
6	3070.5		1223	_	TVCHLV
7		43.0	1308	N	A47253
8	2661		1166	_	S06142
9	2381.5	34.8	1342	N	A36223
10	2300.5	•	1339	N	JC4387
11	1766.5	٠	698	ب	TVFVLV
12	1703	24.9	604		HOAAL
14	1640	24.0	545	N 1	S00727
15	1626.5	23.8	1330	ب	GQFFE
16	1623	23.7	540	N	B44776
17	1621	23.7	540	-4	TVFVEB
18	1478	•	644	N	A36325
19	1276	18.6	1323	N	E88257
21	1194		1369	N 1	S70713
22	1167	•	1717	ب	A45558
23	0		527	N	A42032
24	943.5	٠	843	N	A27131
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585.5	586	587.5	597.5	597.5	601	623	625	630	632.5	645	671	680	683.5	691	701.5
8.6	8.6	8.6	8.7	8.7	8.8	9.1	9.1	9.2	9.2	9.4	9.8	9.9	10.0	10.1	10.3
976	1091	977	984	952	987	2101	1371	1390	2148	1367	1268	1607	1300	1477	1372
N	N	N	2	N	N	N	N	N	۳	مبر	N	N	N	N	N
A36355	S33596	S49004	A39753	I50612	A54092	S57245	A33837	T30346	A56081	IGHUR1	B36502	T43212	A36502	T18534	A34157
protein-tyrosine k	protein-tyrosine k	tyrosine kinase Mp	protein-tyrosine k	protein-tyrosine k	protein-tyrosine k	insulin receptor (insulin-like growt	insulin receptor -	insulin receptor -	insulin-like growt	insulin receptor-r	insulin-like growt	insulin receptor-r	protein-tyrosine k	insulin receptor p

ALIGNMENTS

A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Couss-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Coussens, L.; Yang-Peng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chrore appears on the country of the c A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcription
A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622 A;Molecule type: mRNA
A;Residues: 1-1255 <AM>
A;Residues: 1-1255 <AM>
A;Residues: 1-1255 <AM>
A;Residues: 1-1255 <AM>
A;Residues: 1-1255 <AM>
A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;Coss-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1995
A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid:
A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N;Alternate names: C-erb-B-2 protein precursor; kinase-related transforming protein e:
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1997 #sequence revision 06-Dec-1996 #text_change 11-Jun-1999
C;Accession: A24571; A25491; Ā44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growtl
A;Reference number: A24571; MUID:86118663; PMID:3003577
A;Accession: A24571 A; Molecule type: DNA A: Residues: 1-191 <T/ A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 832-909 <REX> A;Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 737-1031 <SEM>

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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-635/Domain: extracellular #status predicted <EXT>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F;395-605/Domain: intransmembrane #status predicted <TMM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;718-983/Domain: intracellular #status predicted <INT>
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
F;680/124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred
F;753/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
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A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by A1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:120613; OMIM:164870 A;Map position: 17q21.1-17q21.1 A;Introns: 25/1; 75/3; 147/1; 883/3 A;Note: the list of introns is incomplete C;Function:
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;Comment: Amplifica
;Genetics:
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Best Local Similarity
Matches 1224; Conserv
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                                                                                                                                                       DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                           LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                  PWDQLFRFNNFTVSFWLRVPKVSASHLBECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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                                                                                                     PWDQLFRNPHQALLHTANRPE.
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                                           LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                                                                                                                                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                                                                                                                                      YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT
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97.1%;
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overexpression of this erbB-related gene occurs
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Pred. No. 2
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Gene 110, 291-25, 1994
A;Title: Cloning and activation of the Syrian |
A;Reference number: 148161; MUID:94193007; PMII
A;Accession: 148161
A;Status: preliminary; translated from GB/EMBL,
A;Molecule type: mRNA
A;Residues: 1-1254 aRES>
A;Residues: 1-1254 aRES>
C;Genetics:
A;Gene: neu
C;Superfamily: epidermal growth factor receptor
C;Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN:
F;726-734/Region: protein kinase ATP-binding mc
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I48161

p-185 precursor - golden hamster
p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Gene 140, 251-255, 1994
Gene 140, 251-255, 1994
Gene 140, 251-255, 1994
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85.3%; Score 5846.5; DB 2
85.3%; Pred. No. 1.4e-231;
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 APRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVA
                                                                                                                                                                   ALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI
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APVDÍDTNRSRÁCPPCAPACKONHCWGESPEDCQILTGTICTSGCARCKGRLPTDCCHEQ ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ 239

243

124

DPLNNTTPVT-GASPGGIRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL

DPQDNVAASTPGRTPEGLRELQLRSLTEILKGGVLIRGNPQLCYQDMVLWKDVFRKNNQL

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A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphor
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                       P;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Carcinogenesis 12, 1975-1978, 1991
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain 2-thiazolyllformamide or N-methyl-N-nitrosourea.
A;Reference number: A61204, MUID:92035293; PMID:1682063
A;Accession: A61204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) neu precurso C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 C;Accession: A24562; A61204 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. Nature 319, 226-230, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: authors translated the codon GCA for residue 25 as Val \text{C}\text{;}\textsc{Genetics:}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The neu oncogene encodes an epidermal growth fA;Reference number: A24562; MUID:86118662; PMID:3945311A;Accession: A24562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 637-663,'V',665-702 < MAS>
                                                                                                                                                                                                                                               Matches 1084;
                                                                                                                                                                                                                                                                                                                                                        ;882,1227,1253/Binding
                                                                                                                                                                                                                                                                       Local
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        64
                                                                 61
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                  MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
ELTYVPANASLSFLODIOEVOGYMLIAHNQVKRVPLORLRIVRGTQLFEDKYALAVLDNR 123
                                   ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                    MELAAWCRWGFLLALLPPGIAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLACSPQPEYVNQPEVRPQPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGG
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85.8%; Pred. No. 1.4e-231;
tive 52; Mismatches 118;
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                                DVPV
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DVPV
                                                                   ENPEYLVPREGTASPPHPSPAFSPAFDNLYYWDQNSSEQGPPPSNFEGTPTAENPEYLGL
                                                                                                ENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGL
                                                                                                                                         TCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAV
                                                                                                                                                                                                                                   RSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPL
                                                                                                                                                                                                                                                                                                               DDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP
                                                                                                                                                                                                                                                                                                                                                               YMIMYKCWMIDSECRPRERELVSEFSRMARDPQRFVVIQNEDLGFSSPMDSTFYRSLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MR I LKETELRKVKVLGSGAFGTVYKG I WI PDGENVKI PVA I KVLRENTSPKANKE I LDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSSSCVARCPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHFLAGQECVEECRVWKGLPREYVSDKRCLPCHPECQPQNSSETCFGSEADQCAACAHYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGFDEADQCVACAHYK
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                                                                                                                                                                                                                                                                                                                                                                                  YMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQ
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                                                                                                                                                                                                                  RSPLAPSEGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLQRYSEDPTLPLPPETDGYVAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFIIATVEGVLLFLILVVVVGILIKRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQ
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A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
R;Weber, W.; Gill, G.N.; Speiss,
Science 224, 294-297, 1984
A;Reference number: A05281; MUID.
A;Accession: A05281
                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 713-964 cLIN>
A; Residues: 713-964 cLIN>
A; Experimental source: epidermoid carcinoma cell line A4
R; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.;
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A; Reference number: A23062; MUID: 85046483; PMID: 6093780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Rosidues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-3
A;Residues: 'RCAWRRA',150-181,'K',813-942 <XUY>
',798-799,'TD',802-811,'R',813-942 <XUY>
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF rec.
R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma,
Science 224, 843-848, 1984
A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplificatic
A;Reference number: A43615; MUID:84196372; PMID:6326261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-29 <AB29;
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA296
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA296
A;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription & A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672
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GQHUE
GQHUE
GQHUE
GQHUE
epidermal growth factor receptor precursor - human
epidermal growth factor receptor precursor - human
epidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05288;
R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.;
A; Molecule type: p
A; Residues: 25-30,
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A;Title: Characterization and sequence of the promoter region of A;Reference number: A25772; MUID:85270438; PMID:2991899
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A Residues: 1-29 <HAL>
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A; Residues: 1-29 <ISH>
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A; Residues: 1-1210 < ULL>
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A;Title: Functional independence of the epidermal growth factor recept A;Reference number: A3331; MUID:90003233; PMID:2790960 A;Reference number: A33331; MUID:90003233; PMID:2790960 A;References: annotation; internalization signal C;Comment: Binding of EGF to the receptor leads to internalization of C;Genetics: A;Gene: GDB:EGFR A;Cross-references: GDB:120610; OMIM:131550 A;Gene: GDB:EGFR A;Cross-references: GDB:120610; OMIM:131550 A;Map position: 7p12.3-7p12.1 C;Superfamily: epidermal growth factor receptor; protein kinase homo: C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosic;Keywords: ATP; autophosphorylation; duplication; GSTC;F1-24/Domain: signal sequence #status predicted <MATY-F2-645/Domain: extracellular #status predicted <MATY-F2-645/Domain: EGF receptor extracellular domain repeat <EE1>F3-1210/Product: EGF receptor extracellular domain repeat <EE1>F3-100/Domain: EGF receptor extracellular domain repeat <EE1>F3-10-975/Domain: intracellular #status predicted <INT>F3-10-975/Domain: intracellular #status predicted <INT>F3-10-975/Domain: protein kinase homology <KIN\F3-10-975/Domain: protein kinase homology <KIN\F3-10-975/Domain: coated-pit mediated internalization signal F3-124,715,352,413,444,528,603/Binding site: carbohydrate (Asn) (coval F3-745/Active site: Lys #status experimental
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A;Title: Identification of residues in the A;Reference number: A60143; MUID:85182650; A;Accession: A60143
A;Molecule type: protein A;Residues: 740-744,'X', 746-747 <RUS>
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
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                                                 PTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGI
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RESULT A53183

epidermal growth factor receptor precursor - mouse C;5pecies: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999 C;Accession: A53183; A43818; \(\bar{S}24942; \) A28941; \(S45325; \) I49643 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jeu Genes Dev. 8, 399-413, 1994 A;Title: The mouse waved-2 phenotype results from a point mutation in the EC A;Reference number: A53183; MUID:94170986; PMID:8125255 A;Accession: A53183
A;Molecule type: mRNA A;Residues: 1-1210 <LUE> A;Cross-references: GB:U03425

H.S.; Jenkins,

N.A.

EGF

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A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
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A;Gene: EGFR
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C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phos
F;1-24/Domain: signal sequence #status predicted <SIG>
F;48-670/Domain: transmembrane #status predicted <TMM>
F;712-977/Domain: protein kinase homology <KIN>
F;720-728/Region: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;997,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: or 1030 or 1032) phosphate services (Ser) (covalent) #status experimental
F;1028/Binding site: or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
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A;Residues: 1-971, K, 973-1210 <VER>
A;Residues: 1-971, K, 973-1210 <VER>
A;Residues: 1-971, K, 973-1210 <VER>
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1;
A;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor gen
A;Reference number: 149643; MUID:93126380; PMID:7678348
A;Accession: 149643
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A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epidermal Grow A;Reference number: S45325
A;Accession: S45325
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A;Residues: 969-971, 'K', 973-1115,'D' <BIS>
A;Residues: 969-971, 'K', 973-1115,'D' <BIS>
A;Cross-references: EMBL:Z12608
R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
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A; Accession: S24942
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R;Eisinger, D.P.; Serrero, G.
submitted to the EMBL Data Library,
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A;Title: Comparison of EGF receptor sequences as a guide to A;Reference number: A43818; MUID:91232866; PMID:2030916
A;Accession: A43818
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Matches 632
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                                 DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG
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                                                                                                                                                                 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                     -YGTNRTGLRELPMRNLOEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
- OSHPSSCPKCDPSCPNGSCWGGGEENCOKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
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49.4%; Pred. No. 6e-119;
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MGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRS 1079 MVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDDD LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI SAVVGILLVVVLGVVFGI-LIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI ENPEYL-TPQGGAAPQPHPPPAFSPAFDNLYYWDQ-----DP-----TCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAV PLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSET--DGYVAPL 1137 YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI LKETEFKKIKYLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVM LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM TGIVGGLLFIVV-VALGIGLFMRRRHIVRKRTLRRLLQERELVEPLTPSGEAPNQAHLRI CVKTCPAGIMGENNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGCEVWPSGPKIPSIA HAFENLEI IRGRTKOHGOFSLAVVGLNITSLGLRSLKEISDGDVI ISGNRNLCYANTINW MVKCWMIDADSRPKFRELILEFSQMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEED LHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICTIDVYMI RGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPF DQLFRFNNFTVSFWLRVPKVSASHLE-ECVGEGLACHQLCARGHCWGPGPTQCVNCSQFL PLLSSLSATSN----NSTVACINRNGSCRVKEDAFLORYSSDPTGAVTEDNIDDAFL---YLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESI CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV KKLFGTPN-----QKTKIMNNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDCVSCQNVS HFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELBILKTVKEITGFLLIQAWPDNWTDL -FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEBITGYLYISAWPDSLPDL VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFK-DTLSINATNIK LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELE CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY RGRECVEKCNILEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPH CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY PTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPN PERGAPP 1019 1034 1008 948 960 888 900 828 840 780 661 601 768 708 720 649 590 530 477 303 541 482 417 357

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A;Gene: erbB
A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
pecific protein kinase
F;1-30/Domain: signal sequence #status predicted <SIG>F;31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
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F;31-654/Domain: extracellular #status predicted <ESIN>
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F;678-1223/Domain: intracellular #status predicted <IMTN>
F;719-984/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase homology <KIN>
F;136,202,280,361,370,422,575,580,615,655/Binding site: carbohydrate (Thr) (covalent) #sfinding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;6754/Rotive site: Lys #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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A; Residues: 1-1223 <LAX>
A; Cross-references: GB:M20386
R; Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Ra Cell 41, 719-726, 1985
A; Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing A; Accession: A00643; MUID:85228222; PMID:2988784
A; Accession: A00643
A; Molecule type: mRNA
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A;Tille: Chicken epidermal growth factor (EGF) receptor: A;Reference number: A27720; MUID:88261272; PMID:3260329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
;Species: Gallus gallus (chicken)
;Date: 28-Feb-1986 #sequence revision 05-May-1995 #text_change 04-Feb-2000
;Accession: A27720; A00643
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;Residues: 585-1223 <NIL>
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TELE-FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDS
                                                PHNYVVTDHGSCVRSCNTDTYEV-EENGVRKCKKCDGLCSKVCNGIGIGELKGILS-INA
                                                                                                   PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGI
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                                                       YNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLAKTVFESSPYWIQ
                                                                                                                                                                            ---SRTPLLSSLSATSNNSATNCID-
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SGNHQINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                                                                                                                ESIDDGFL-----PAPEYVNQ--LMPKKPS------TAMVQNQI 1118
                                                                                                                                             ET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGV 1186
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                                                                           ----AFGGAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQ 1231
                        -RGAPPSTFKGTPTAENPEYLGLDVP 1260
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epidermal growth factor receptor, HER4 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-C;Date: 0.5 C;Date: 21-253 C;Accession: A47253 R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J.M.; Carlton, Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993 A;Title: Ligand-specific activation of HER4/p180erb84, a fourth member

#text_change 18-Jun-1999

a fourth member of the

epiderma

G.W.;

RESULT A47253

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A;Reference number: A47253; MUID:93189574; PMID:8383326
A;Accession: A47253
A;Accession: A47253
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1308 <PLO>
A;Roross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A;Note: sequence extracted from NCBI backbone (NCBIP:126842)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor;
F;716-981/Domain: protein kinase homology <KIN>
F;724-732/Region: protein kinase ATP-binding motif
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                                                   KEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLN
                                                                                                    TAPNOAOLRILKETELKRVKVLGSGAFGTVYKGIWVPEGETVKIPVAIKILNETTGPKAN
                                                                                                                                                                      AR-TPL--IAAGVIGGLFILVIVGLTFAVYVRRKSIK-KKRALRRFL-ETELVEPLTPSG
                                                                                                                                                                                                      QRASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSG
                                                                                                                                                                                                                                                                                                                                                                                                                   QLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFSNLVTIGGRVLYSGLSLLILKQQGITSLQFQSLKEISAGNIYITDNSNLCYYHTINWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLMSAQTVDSSNIDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY
WCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKV
                                                                                                                                                                                                                                       VEKCPDGLQGANSF--IFKYADPDRECHPCHPNCTQGCNGPTSHDCIYYPWTGHSTLPQH
                                                                                                                                                                                                                                                                              VARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGC
                                                                                                                                                                                                                                                                                                              RICIESCNLYDGEFREFENGSICVECDPQCEKMEDGLLTCHGPGPDNCTKCSHFKDGPNC
                                                                                                                                                                                                                                                                                                                                                                                  TLFSTIN-----QRIVIRDNRKAENCTAEGMVCNHLCSSDGCWGPGPDQCLSCRRFSRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVWVSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEITS
                               VEFMDEALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLN
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Pred. No. 4.7e-113;
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A;Map position: Y
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrar F;1-25/Domain: signal sequence #status predicted <STGs F;26-1166/product: kinase-related transforming protein (Tu) #status pred: F;707-972/Domain: protein kinase homology <KIN>F;715-723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish N;Alternate names: epidermal growth factor receptor homolog; kinase-related C;Species: Kiphophorus maculatus (southern platyfish) C;Date: 10-Sep-1999 #Bequence_revision 10-Sep-1999 #text_change 18-Feb-2000 C;Accession: S06142; S13809 R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989 Rature 341, 415-421, 1989 A;Reference number: S06142; MUID:90015140; PMID:2797166 A;Accession: S06142; MUID:90015140; PMID:2797166
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A;Title: Transcriptional activation of the
A;Reference number: S13807; MUID:91125882;
A;Accession: S13809
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S06142
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A;Residues: 821-1025 'N',1027-1098,'A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1166 <WIT>
A;Cross-references: EMBL:X16891; NID:g65290;
R;Adam, D.; Maeueler, W.; Schartl, M.
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Best Local
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  38.9%;
Score 2661;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                    melanoma inducing PMID:1846957
1; DB 1;
1.3e-101;
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                    Length 1166;
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940 VYMIIKCWMIDPSSRPREFIELVGEFSQMARDPSRYLVIQGNLPSLSDRRLFSRLLS 996 1017 DDDMGDLVDAEEVLVPQQGFFCPDPAPGAGGMVHHRHRSSTRSGGGDLTLGLEPSEEEA 1076	7 0	IKWMA 89	777 AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA 836	700 FLRILKETEFKKDRVLGSGAFGTVYKGLMNPDGENIRIPVALKVLREATSPKVNQEVLDE 759	LTSIVSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTESGAMPNQA 71 :	597 KDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP 656	537 CSQFLRGQECYEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHY 596	477 VHTVPWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVN 536	418 SLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLCF 476 ::	359 ITEL-EPAGCKKIFGSLAFLPESFDGDPASNTAPLOPEQLQVFETLEEITGYLYISAWDD 417 	299 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIG 358	239 QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA 298 : :	180 ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE 238	120 GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTIIMKDIFHKNNQL 179 : : :	60 LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119 :	4 AALCRWGLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59 :	'571; Conservative 167; Mismatches 390; Indels 146; Gaps
QY 188 RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG 246 - -	128 126	68 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT	OY 10 GLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT 67	atch 34.8%; Score 2381.5; DB 2; Length 1342; cal Similarity 39.9%; Pred. No. 3.7e-90;	A; Map position: 12q13-12q13 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo C; Keywords: ATP; phosphotransferase F; 707-972/Domain: protein kinase homology <kin> F; 715-723/Region: protein kinase ATP-binding motif</kin>	A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1; PID:g306841 C;Genetics: A;Gene: GDB:ERBB3; HER3 A;Gene: GDB:ERBB3; HER3 A;Cross-references: GDB:119880; OMIM:190151	eliminary; translated from GB/EMBL/DDBJ ype: mRNA 1-559, G', 561-957, F', 959-1063, G', 1065-1342 <res< td=""><td>Riftowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G. Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990 A; Title: Molecular cloning and expression of another epidermal growth factor receptor-A; Reference number: I59164; MUID:90311312; PMID:2164210 A; Accession: I59164</td><td></td><td>A:Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Accession: A36223; MUID:90083234; PMID:2687875 A;Accession: A36223; MUID:90083234; PMID:2687875</td><td>C;Species: Homo sapiens (man) C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 C;Accession: A36223; I59164 R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.</td><td></td><td>Db 1143 GMFLPAAENLEYLG 1156</td><td>1108 QNSLPLVSSGSN</td><td>1056EYVNQPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTN</td><td>1020EPCIPTGH</td><td>Qy 1077 PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVA 1135</td></res<>	Riftowman, G.D.; Whitney, G.S.; Neubauer, M.G.; Green, J.M.; McDonald, V.L.; Todaro, G. Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990 A; Title: Molecular cloning and expression of another epidermal growth factor receptor-A; Reference number: I59164; MUID:90311312; PMID:2164210 A; Accession: I59164		A:Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal A;Reference number: A36223; MUID:90083234; PMID:2687875 A;Accession: A36223; MUID:90083234; PMID:2687875 A;Accession: A36223; MUID:90083234; PMID:2687875	C;Species: Homo sapiens (man) C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000 C;Accession: A36223; I59164 R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.		Db 1143 GMFLPAAENLEYLG 1156	1108 QNSLPLVSSGSN	1056EYVNQPGSETSSRLSDIYNPNYEDLTDGWGPVSLSSQEAETNFSRPEYLNTN	1020EPCIPTGH	Qy 1077 PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTV-PLPSETDGYVA 1135

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                                                                 NPEYL 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKTHLTWALTVIAG--LVVIFMMLGGTFLYWRGRRIONKRAMRRYLERGESIEPLDPS-E
                                                                                                             MNRRRRHSP-PHPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDE
                                                                                                                                                                  LTPQGGAAPQPHPPPAFSPAFDNLYYWD------
                                                                                                                                                                                                              PPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDED------EEYBY
                                                                                                                                                                                                                                                                                                               PRGCLASESSEGHVTGSEAELQEKVSMCRSRSRSRSPRPRGDSAYHSQRHSLLTPVTPLS 1147
                                                                                                                                                                                                                                                                                                                                                                 P-----SETDGYVA------PLTCSPQPE----YVNQPDVRPQPPSPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KANKVLAR I FKETELRKLKVLGSGVFGTVHKGVWI PEGESIKI PVCIKVI EDKSGRQSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDGPHCVSSCPHGVLG--AKGPIYKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLI
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                    1263
                                                                                                                                                                                                                                                             -LPAARPAGATLERAKTLSP-GKNGVV-----KDVFAFGGAVENPEY
                                                                                                                                                               QDPPERGAPPSTFKGTPTAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
A; Gene: ErbB3
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hellyer, N.J.; Kim, H.H.; Greaves, C.H.; Sierke, S.L.; Kol Gene 165, 279-284, 1995
A;Title: Cloning of the rat ErbB3 cDNA and characterization A;Reference number: JC4387; MUID:96096535; PMID:8522190
A;Accession: JC4387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; growth factor receptor; liver; phosphoprotein; transmembrane prot F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1339/Product: epidermal growth factor homolog #status predicted <MAT>
F;640-659/Domain: transmembrane #status predicted <TMM>
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F;713-721/Region: protein kinase ATP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U29339; NID:g915389; PID:g915390
A;Experimental source: liver
A;Note: The authors translated the codon AAC for residue 369 as Thr and GTT
C;Comment: This protein is a functional heregulin receptor that transduces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-1339 <HEL>
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Best Local :
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530 GPTQCVNCSQFLRGQECVEECRVLQGLPRBYVNARHCLPCHPECQPQNGSVTCFGPBBADQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                           CPHNEV-VDQTECVRACEPDKMEVD-KHGLKMCEPCGGLCPKACEGTGSGSRYQTVDSSN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECAGGCSGPQDTDCFACRFNDSGACVPRCPEPLYYNKLTFQLEPNPHTKYQYGGVCVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAEIVVKNNGANCPPCHEVCKG-RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LNYNT----NSSHALRQLKFTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL
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                                                                                                                           FVHTVPWDQLFRFNNFTVSFWLRVPKVSASHLE-----BCVGEGLACHQLCARGHCWGP
                                                                                                                                                                                                                           DSLPDLSVFQNLQVIRGRILHNGAYS-LTLQGLGISWLGLRSLRELGSGLALIHHNTHLC
                                                                                                                                                                                                                                                                                                             IGITELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVPETLEEITGYLYISAWP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGL--GMQYIKANSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEIVLTGHNADLSFLQWIREVTAYVLVAMNEFSVLPLPNLRVVRGTQVYDGKFAIFVM---
                                                                                                                                                                          PHMHNFSVFSNLTT1GGRSLYNRGFSLLIMKNLNVTSLGFRSLKEISAGRVYISANQQLC
                                                                                                                                                                                                                                                                                ID----GFVNCTKILGNLDFLITGLNVDPWHKIPALDPEKLNVFRTVREITGYLNIQSWP
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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus
N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 11-Jun-1999
C;Cate: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 11-Jun-1999
C;Cate: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 11-Jun-1999
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                                                                                        RAKTLSPGKNGVVKDVF-----
                                                                                                                                            RYSEDPTVPLPSET---DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE
                                                                                                                                                                                                                                                             PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG
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KTVFESSPYWIOSGNHOINLDNPDYQQDFLPNETKPNGLLKVPAAENPEYLRVAAP
                             SPAFDNLYYWDQ------DPPE-----RGAPPSTFKGTPTAENPEYLGLDVP
                                                                                                                     RYSSDPTGNFLEESIDDGFL----PAPEYVNQ--LMPKKPS-----
                                                                                                                                                                                                        GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
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                                                         -TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL-----NTNQSPLA
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; Pred. No. 2.5e-65;
80; Mismatches 137;
                                                                                        ----AFGGAVENPEYLTPQGGAAPQPHPPPAF 1219
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protein-tyrosine kinase (EC 2.7.1.112) erbB - avian ery C; Species: avian erythroblastosis virus C;Date: 18-Apr-1984 #tex C;Accession: A00644; A38022 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; C Cell 35, 71-78, 1983 A;Title: The erbB gene of avian erythroblastosis virus A;Reference number: A00644; MUID:84026539; PMID:6313229 A;Accession: A00644 A;Accession: A00644 A;Accession: A00644 A;Accession: GB:K01216; NID:g209676; PIDN:AAA424 A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA424
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Saule,

Martin,

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R;Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, Science 224, 1456-1459, 1984
A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a i A;Reference number: A38022; MUID:84223957; PMID:6328658
A;Accession: A38022
A;Accession: A38022
A;Molecule type: DNA
A;Residues: 1-28, 'W', 30-139, 'F', 141-145,' V', 147-152 <DEB>
A;Cross-references: GB:KO2006
C;Genetics:
A;Cross-references: GB:KO2006
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: protein kinase ATP-binding motif
F;130-395/Domain: protein kinase ATP-binding motif
F;165/Active site: Lys #status predicted
RESULT 13
S35745
protein-tyrosine |
C;Species: avian
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                                                                                     SSPYWI
                                                                                                               NLYYWDODPPERGAPPSTFKGTPTAENPEY 1254
                                                                                                                                                                          NGVVKDVFAF--
                                                                                                                                                                                                                                                                                                                                      YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
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                                                                                                                                          --- VQNQIYNFISLTAISKLPMDSRYQNSHSTAVDNPEYL----
                                                                                                                                                                                                                                                          -----SRTPLLSSLSATSNNSATNCID------RNGQGHPVREDSFVQRYSSDPTGN
                                                                                                                                                                                                                                                                                     PSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVP 1125
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                                                                                                                                                                                                                                                                                                                    YRTLMEEEDMEDIVDADEYLVPHQGFF------NSPST-------
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kinase (EC 2.7.1 erythroblastosis
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llarity 52.2%;
Conservative 76
             2.7.1.112) erbB
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Pred. No. 8.5e-63;
6; Mismatches 128;
                                                                                                                                                                      ---GGAVENPEYLTPQGGAAPQPHPPPAFSPAFD
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             erythroblastosis
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrc
F;135-40()Domain: protein kinase homology <KIN>
F;143-151/Region: protein kinase ATP-binding motif
F;170/Active site: Lys #status predicted
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A,Accession: S35745
A,Molecula F---
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C;Accession: S35745
R;Vennstroem, B.
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A; Residues: 1-544 < VEN>
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                                                                                                                                                                            PASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSG
                                                                                                                                                                                                                                                                                                                                            LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
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                            AKTLSPGKNGVVKDVFAFGGAVENPEYL
                                                                                                                                  GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ 1116
                                                                                                                                                              LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF----
                                                                                                                                                                                                                                  KGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLG
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                                                       -LMPKKPSTAMVQNQIYNYISLTAISK
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RESULT 14
S00727
kinase-related transforming protein (erbB)
C;Species: avian erythroblastosis virus
C;Date: 01-Dec-1989 #sequence_revision 01-F
C;Accession: S00727
R;Scotting, P:; Vennstrom, B:; Jansen, M.;

01-Dec-1989

#text_change

EC

2.7.1.-) -

avian

Graf,

7.;

Beug,

Η.,

Hayman, 28-Feb-1997 erythroblastosis

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epidermal growth factor receptor - fruit fly (Drosophila melanogaster) N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Drosophila melanogaster C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 11-Jun C;Accession: A00640; A38021 R;Livneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z. Cell 40, 599-607, 1985
                                                                                                                                      RESULT
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A;Title: Common site of mutation in the erbB gene of avian erythroblastosis A;Reference number: S00727; MUID:88217326; PMID:2897102
A;Accession: S00727
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Residues: 1-545 <SCO>
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     Drosophila
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                                                                                                                                                                                                                                    AKTLSPGKNGVVKDVFAFGGAVENPEYL
                                                                                                                                                                                                                                                                                                 RYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGAT-LER 1175
                                                                                                                                                                                                                                                                                                                                                               GGDLTLGLEPSEEEAPRSPL----APSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQ
                                                                                                                                                                                                                                                                                                                                                                                                      LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF----
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     EGF receptor
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Pred. No. 2.9e-60;
9; Mismatches 122;
     gene
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   homolog:
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A;Residues: 'A',832-866,'V',868-943,'QTPSLVK' <WAD>
A;Residues: 'A',832-866,'V',868-943,'QTPSLVK' <WAD>
C;Comment: This sequence is tentative because the introns have not been in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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A;Accession: A00640
A;Molecule type: DNA
A;Residues: 1-1330 <LIV>
A;Cross references: EMBL.K03054
R;Wadbworth, S.C.; Vincent III, W.S.; Biloc
Nature 314, 178-180, 1985
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SLTIERARYAIQSAGLAMELEQITARSASMRHSKTLPAEGRQVPRWVFLGVCASARAGIA
                                                                                                                                                                                                              SNIRWPAIQKEPEQKVWVNENLRADLCGKFLTILISVQHNIIMHIFAICREKWNHLLGSV
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                                                                                                    QRGRLLGSWHGSVPYLQELQFQWHLHRRLWLYIQVSINSTQDKSNEHQLTDACYSPSVPT
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                                                                                                                                                                                                                                                                                                                          -DMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP 1077
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Result
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ERBB_AVIEU
EGFR_CHICK
LT23_CAEEL
ERB2_MOUSE
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INSR_RAT
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IRR_HUMAN
IRR_ALDAE
IGIR_MOUSE
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P14616 homo sapien
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P14617 lymnaea sta
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P24062 rattus norv
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Q01279 mus musculu
Q15303 homo sapien
Q62956 rattus norv
P13388 xiphophorus
P21860 homo sapien
Q62799 rattus norv
P04412 drosophila
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3 homo sapien
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R InterPro; IPR002174; Furin-Line.

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DR InterPro; IPR004019; YLP motif.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF00757; YLP; Z

DR Pfam; PF00757; YLP; Z

DR ProDom; PD000001; Euk_pkinase; 1.

DR ProDom; PD000001; Euk_pkinase; 1.

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DR PROSITE; PS00117; PROTEIN_KINASE_TOM; 1.

DR PROSITE; PS00119; PROTEIN_KINASE_TOM; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_TOM; 1.

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POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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RESULT 2
ERB2_RAT
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p06494;
p01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2 (p185erbB2) (NEU protein-concogene) (C-erbB-2) (Epidermal receptor-related protein).
                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Neuroblastoma;
MEDLINE=86118662; PubMed=3945311;
Bargmann C.I., Hung M.-C., Weinberg
"An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                   SEQUENCE OF 852-905 FROM N.A.
TISSUE-Sciatic nerve;
MEDLINE-91222560; PubMed-2025425;
Lai C., Lemke G.;
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
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SMART; SM00229; TyrKC; 1.

PROSITE; PS000107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_TOM; 1.

Transmembrane; Glycoprotein; Multigene fi
Transferase; Tyrosine-protein kinase; ATI
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MEDLINE-92155181; PubMed1346763;

Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G.,

Newman R., Crumpton M.J., Sternberg M.J.B., Campbell

"Three dimensional structure of the transmembrane reg
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HSSP; P11362; 1FGK
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EMBO J. 11:43-48(1992).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEWREGULIN-RECEPTOR COMPONENT OF A NEW FORTH IT ALONE. GP30 POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, ALPHA AND AMPHIREGULIN.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + protein tyrosine = ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP + ADP
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Pfam; PF00757; Furin-like;
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InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR004019; YLP_motif.
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SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPT
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A
SUBCELLULAR LOCATION: Type I membrane protein.
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Q60553;
Q60553;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Receptor protein-tyrosine kinase erbB-2
(p185erbB2) (NEU proto-oncogene) (C-erbF
ERBB2 OR NEU
             Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Aidi M., Yamazaki Y., Ishikawa T., Yamazaki Y., Ishikawa T., "Cloning and activation of the Syrian hamster neu proto-oncogene.", Gene 140:251-255 (1994).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-I- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                        MEDLINE=94193007; PubMed=7908275;
Nakamura T., Ushijima T., Ishizaka
Yamazaki Y., Ishikawa T.;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM
TISSUE=Nerve;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10036;
SUBCELLULAR LOCATION: Type I membrane PTM: LIGAND-BINDING INCREASES PHOSPHOF
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InterPro; IPR000494; EGFR L domain.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR0002174; Furin-like.

InterPro; IPR001214; Furin-like.

InterPro; IPR001214; Furin-like.

InterPro; IPR001219; YLP_motif.

Pfam; PF00069; pkinase; 1.

Pfam; PF000757; Furin-like; 1.

Pfam; PF001030; Recept_domain; 2.

Pfam; PF000757; YLP; 2.

IR Pfam; PF002757; YLP; 2.

IR Pfam; PF002757; YLP; 3.

SWART; SM00261; FU; 3.

SWART; SM00219; TyrKc; 1.

IR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

IR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

IR PROSITE; PS00109; PROTEIN KINASE_DOW; 1.

IR PROSITE; PS00101; PROTEIN KINASE_DOW; 1.

Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

"Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

"Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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Similarity 85...
80; Conservative
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DVYMIMVKCWMIDSECRPRERELVSEFSRWARDPORFVVIQNEDLGPSSPLDSTFYRSLL
                   DVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLL
                                                        ALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI
                                                                                                                      AKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKMM
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                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=97256547; PubMed=9103388;
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(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95382957; PubMed=7654368; Ilekis J.V., Stark B.C., Scoccia B.; Tlekis J.V., Stark B.C., Scoccia B.; The regulation "Possible role of variant RNA transcripts in the regulation epidermal growth factor receptor expression in human placent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=84219729; PubMed=6328312;
Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor cDNA sequence and aberrant
expression of the amplified gene in A431 epidermoid carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGFR HUMAN STANDARD; PRT; 1210 AA. P00533; P06268; Q14225; Q9UMD7; Q9UMD8; Q9UMG O00688; Q9BZS2; Q9H2C9; Q9GZX1; Q9H3C9; Q1-JUL-1986 (Rel. 01, Created) o1-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (Epidermal growth factor receptor precursor (
TISSUE=Placenta;
MEDLINE=21100872;
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                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic
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MEDLINE=97078686; PubMed=8918811;
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Nature 309:418-425(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                       "Lekis J.V., Gariti J., Niederberger 
"Expression of a truncated epidermal 
protein (TEGFR) in ovarian cancer.", 
Synecol. Oncol. 65:36-41(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                            kb alternative transcript from the receptor gene encodes a truncated c Acids Res. 24:4050-4056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.L., Maihle N.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLDVPV
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Lampland A.L., Balasubramaniam S
Maihle N.J.;
"Human and mouse alternative EGF!
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Roe B.A., Merlino G.T., Pastan I.;

"Human epidermal growth factor receptor cDNA is
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Nature 309:806-810(1984).
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MEDLINE=88217333; PubMed=3329716;
Mittle N., Bennett P.,
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Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
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"Expression cloning of human Egf receptor RNA products in A4"
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IBhil S., Xu Y.H., Stratton R.H.,
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                                                                                                       Submitted
                                                                                                                                              SEQUENCE
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"The human EGF receptor gene: structure identification of sequences regulating Oncogene Res. 1:375-396(1987).
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receptor cDNA from
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Commun. 124:125-132(1984)
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-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1/p170 (shown here), 2/p truncated isoform/TEGFR, 3/p110 and 4; are produced by alternative splicing.

-!- TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is al expressed in ovarian cancers.

-!- MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carpenter G.; "Receptors for epidermal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96398132; PubMed=8962717; Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.; Which K.D., Davies G., Bailey D., Renouf D.V., Hounsell E.F.; "Analysis of the glycosylation patterns of the extracellular domain the epidermal growth factor receptor expressed in Chinese hamster ovary fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M. Howk R., Givol D., Ullrich A., Schlessinger J.;
"All autophosphorylation sites of epidermal growth factor (EG receptor and HER2/neu are located in their carboxyl-terminal Identification of a novel site in EGF receptor.";
J. Biol. Chem. 264:10667-10671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitogens.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87297456;
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                                                                                           s SWISS-PROT entry is copyright. It is produced through a collai ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in this day of the statement is not removed. Usage by and for content in the statement is not removed. Usage by and for content in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                   U. Rev. Biochem. 56:881-914(1987).

FUNCTION: Receptor for EGF, but also for other members of the Efamily, as TGF-alpha, amphiregulin, betacellulin, heparin-bindi EGF-like growth factor, GP30 and vaccinia virus growth factor. involved in the control of cell growth and differentiation.

FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               supercoiled DNA.";
ire 309:270-273(1984).
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Odaka M., Inagaki F., Lax I., Schlessinger J., Kohda
ide bond structure of human epidermal growth factor re
. Chem. 273:11150-11157(1998).
                                                                 requires a license agreement
an email to license@isb-sib.cl
; CAA25240.1;
; AAB53063.1;
; AAC50802.1;
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., Abe Y., Saito K.,
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                                                   EDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILR
                                                                                             VGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYL
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STRAIN-B6/C3, TISSUE=Liver;
MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGFR MOUSE
Q01279;
01-FEB-1996
                                                                                                                                                                                                                                  Hibbs M.L.;
Submitted (APR-1994)
                         MEDLINE=91232866;
                                         TISSUE=Brain;
                                                         SEQUENCE
                                                                                                                                                                                                                                                                STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                Paria B.C., Das S.K., Andrews G.A., Dey C...., Paria B.C., Das S.K., Andrews G.A., Dey C...., Paria B.C., Das S.K., Andrews G.A., Dey C..., Property of the epidermal growth factor receptor in mouse blastocysts during delayed implantation.", Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c, and CD-1; TISSUE=Liver, MEDLINE=93126380; PubMed=7678348; Medraus B.C., Das S.K., Andrews G.K., De
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MEDLINE=93026370; PubMed=1408137;
Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Mammalia;
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15-JUN-2002
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                                                                                     tyrosine kinase.";
v. 8:399-413(1994).
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the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
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                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
or send an email to license@isb-sib.ch).
                       entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparison of EGF receptor binding site."; Oncogene 6:673-676(1991).
                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation synthesis, and cell proliferation.
                                                                                                                                                                                                                                                                                                                                mitted (JUN-1992) to the EMBL/GenBank/DDBJ databases. FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEBPARIN-BINDING EGF, GP: VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY). CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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Q15303;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.
(p180erbB4) (Tyrosine kinase-type cell surface receptor
ERBB4 OR HER4.
Homo sapiens (Human).
SEQUENCE FROM N.A. (ISOFORM JM-A). TISSUE=Breast carcinoma;
TISSUE=Breast carcinoma;
MEDLINE=93189574; Pubmed=8383326;
Plowman G.D., Culouscou J.-M., While
Foy L., Neubauer M.G., Shoyab M.;
"Ligand-specific activation of HER-
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates;
of HER4/p180erbB4,
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                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
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SMART; SMO0261; FU; 4

SMART; SM00261; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS001107; PROTEIN_KINASE_TYR; 1

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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J. Biol. Chem. 2'
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HSSP; P11362;
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Klagsbrun M.;
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MEDLINE=97476287; P
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                                                                                                                                                                                                                                                                                                                   InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PITUITARY, SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS, LUNG, SALIVARY GLAND, AND PANCREAS.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;

ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN
CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JIOLI Chem. 272:26761-26768(1997).

3101. Chem. 272:26761-26768(1997).

FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-UNRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, BETACELLULIN AND NAME. INTERACTION WITH THESE FACTORS INDUCES CELL DIFFERENCIATION.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.

NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
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SUBUNIT: HOMODIMER OR HETERODIMER WITH EACH OF
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                                                                                                                                                                                                                                                PF00069; pkinase; 1.
PF00757; Furin-like; 1.
PF0130; Recep L domain;
PF02757; YLD;
PF02757; YLD;
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IPR000719; Euk pkinase.
IPR002174; Furin-like.
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Sci. U.S.A. 90:1746-1750(1993)
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s G., Paul S., Choi C.J.,
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 PROTEIN KINASE
                                                                                                                                   kinase;
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ATP-binding; Phosphorylation;
                                                                                       PROTEIN-TYROSINE
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    EMBL; AF041838; AAD08899.1; ...
EMBL; U92531; AAC53051.1; ...
HSSP; P11362; 1FGK.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkīnase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR00145; Tyr pkinase.
InterPro; IPR004019; YLP motif.
Pfam; PF00075; Furin-like; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF01030; Recep L domain; 2.
Pfam; PF01030; Tyr pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Sciatic nerve;
MEDLINE=91222560; PubMed=2025425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Neuregulins promote survival and growth of cardiac myocytes. Persistence of ExbB2 and ExbB4 expression in neonatal and adventricular myocytes.";
J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last
Receptor protein-tyrosine
ERBB4 OR TYRO-2.
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STRAIN=Sprague-Dawley; TISSUE=Spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao Y.-Y., Sawyer D.R., Baliga R.R., Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97184212; PubMed=9030624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lai C., Lemke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98221155; PubMed=9553078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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RESIDUES
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SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTE OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN TRETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY,
                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                            HEART
                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                 PR00109; TYRKINASE
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                                                                                                                                                                                                                                                                                                                                                                                            LIGAND-BINDING
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Euk_pkinase;
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Rodentia;
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kinase erbB
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Sciurognathi; Muridae;
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SMART; SM00219; TyrKc; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN KINASE_TYR; 1.

TYPARMEMBERS PS00109; PROTEIN KINASE_TYR; 1.

TYPARMEMBERS PROTECTION KINASE; ATP-binding; Phosphorylation.
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01-JAN-1990 (Rel. 1
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                                                                                                                                                                                                                                                                                                          InterPro; IPR000494; EGFR L domais
InterPro; IPR000719; Euk pkinase.
InterPro; IPR002174; Furin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MELANOMAS
-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schartl M.;
Submitted (JUL-2000)
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Eukaryota; Metazoa; Chordata; Craniata; Puteleos

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neorele

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Coprinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inducing Tu locus in Xiph Nature 341:415-421(1989).
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MEDLINE=90015140; PubMed=2797166;
Wittbrodt J., Adam D., Malitschek
Telling A., Robertson S.M., Schart
                                                                                                                                                                                                                                                                        InterPro; IPR002290; Ser_thr_pkinase.
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FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + prot
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S; PR00109; TYRKINASE.
m; PD000001; Euk_pkinase;
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PF00757; Furin-like; 1.
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Pred. No. 7.1e
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                                                 01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC (C-erbB3) (Tyrosine kinase-type cell surface receptor
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                  ERB3
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                                       ERBB3 OR HER3
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Catarrhini; Hominidae
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   Hominidae;
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InterPro; IPRO00494; EGFR L domain.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR000719; Furin-like.

InterPro; IPR0001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00069; pkinase; 1.

DR Pfam; PF00757; Furin-like; 1.

DR Pfam; PF00001; Euk_pkinase; 1.

DR Pronom; PD000001; Euk_pkinase; 1.

DR SMART; SM00261; FU; 3.

DR SMART; SM00219; TyrKG; 1.

DR SMART; SM00219; TyrKG; 1.

DR PROSITE; PS00110; PROTEIN_KINASE_TYR; FALSE_NEG.

DR PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                         EMBL; M29366; AAA35790.1; -.
EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB26935.1; -.
PIR; A36223; A36223;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
MEDLINE=90311312; PubMed=2164210;
Plowman G.D., Whitney G.S., Neubauer M.G., Green J.
Plowman Shoyab M.;
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"Isolation and characterization of ERBB3, a third member
ERBB/epidermal growth factor receptor family: evidence fc
overexpression in a subset of human mammary tumors.";
Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
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"Molecular cloning and expression of factor receptor-related gene.";
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                                      Pfam; PF00069; pkinase; 1.
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Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF000001; Recep_L domain; 2.
PRINTS; PR00109; TYRKINASE;
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00261; FU; 5.
SMART; SM00219; TYFKC; 1.
SMART; SM00019; PFC5IN KINASE
PROSITE; PS00109; PROTEIN KINASE
PROSITE; PS0011; PROTEIN KINASE
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Q62759; Q62955;
15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                 EMBL; U29339;
EMBL; U52530;
HSSP; P11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE=96096535; PubMed=8522190; Hellyer N.J., Kim H.-H., Greaves C.H "Cloning of the rat ErbB3 cDNA and clrecombinant protein.";
                                                                                                                                                                                                                                                                        InterPro; IPR000494; EGFR L domain.
InterPro; IPR000719; Euk pkīnase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
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Mammalia; Eutheria;
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DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIL
AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF
PHOSPHATIDYLINOSITOL 3-KINASE.
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SUBUNIT: HETERODIMER WITH EACH OF
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; AAC53050.1; -.
; 1FGK.
                        Glycoprotein;
TYPKC; 1.

IYPKC; 1.

FROTEIN KINASE ATP; FAL

FROTEIN KINASE TYR; 1.

FROTEIN KINASE DOM; 1.

FROTEIN KINASE DOM; 1.
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Rodentia;
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Sciurognathi; Muridae;
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                family; Receptor; Signal;
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EGFR_DROME STANDARD; PRT; 1426 AA.
P04412; O61601; Q9W2G0; P81868;
113-AUG-1987 (Rel. 05, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Epidermal growth factor receptor precursor (EC 2.7.1.112)
(Gurken receptor) (Torpedo protein) (Drosophila relative o
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfeinnkoch C., Baldwin D.,
RA Belew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McImmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                    MEDLINE=99102120; PubMed=9882502;
Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila
Dev. Biol. 205:129-144(1999).
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"Alternative 5' exons and tissue-specific expression
Drosophila EGF receptor homolog transcripts.";
Cell 46:1091-1101(1986).
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                EMBL;
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                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                           UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX AND THORACIC AND ABDOMINAL CANOTITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 89:13-16 (1997).

FONCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAMAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.

CRITICAL FOR THE PROLIFERATION OF INAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ENTERO-POSTERIOR AND DORSO-VENTEAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF ANNIOSEROSA AND VENTRAL NETWORCTODERMAL CELLS, GERM BAND RETRACTION, CELL FA AND VENTRAL CELL FATES, WAINTENANCE OF ANNIOSEROSA AND VENTRAL NETWORCTODERMAL CELLS, GENERAL BAND PRODUCTION OF
C; AF052754; AAC08536.1; -.

C; AF052753; AAC08536.1; JOINED.

C; AF052754; AAC08535.1; -.

C; AF052752; AAC08535.1; JOINED.

C; K03054; AAAS1462.1; -.

C; K03417; AAAS1460.1; -.
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE),
TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS.
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SUBCELLULAR LOCATION: ISOFORMS
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PROSITE; PS00107; PROTEIN_KINAS
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Tyrosine-protein kinase; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MBL; AF109082; AAD26132.1; JOINED.
MBL; AF109078; AAD26133.1; -
MBL; AF109078; AAD26133.1; JOINED.
MBL; AF109079; AAD26130.1; -
MBL; AF109079; AAD26130.1; JOINED.
MBL; AF109081; AAD26131.1; JOINED.
MBL; AF109081; AAD26131.1; JOINED.
MBL; AF109080; AAD26131.1; -
MBL; AF009080; AAD26135.1; -
MBL; AF009080; AAD26135.1; -
MBL; X78919; CAAS5523.1; -
MBL; X78919; CAAS5522.1; -
MBL; X78919; CAAS5522.1; -
MBL; X78919; CAAS5522.1; -
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MBL; X78919; CAAS522.1; -
MBL; X78919; CAAS
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K03418;
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AF109078; AAD26132.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITEL-----
                                                        KNFFDEAVSKEECPPMRKYNPTTYVLETN
                                                                                                                                                                                                        MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                               YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                                                                                                                                                                                                                                       RELOLRSLTEILKGGVLIQRNPOLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP
                                                                                                                                                                                                                                                                                                                                                                                               YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVLIAHNQVRQVPLQRLRIVRGTQLF-----EDNYALAVLDNGDPLNNTTPVTGASPGGL
                                                                                                                LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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AAA51461.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                               CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC
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952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in; Receptor ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1920;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIDERMAL GROWTH EXTRACELLULAR (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                        GHLLRDNGACVRSC
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EFAGCKK
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                                 ENPEYL --- TPQGGAAPQPH ---
                                                                                                                                                                                                                                                                                                                               LAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVVFGILIKRRQQKIRKYT--MRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKV
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                                                                                                                                                               SNKNSSTGDDERDSSAREVGVGNLR
                                                                                                                                                                                                 LAPSEGAGSDVFDG----DLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPL 1137
                                                                                                                                                                                                                                                SEATAKPODYLQPKAAPGPS----HRTDCT
                                                                                                                                                                                                                                                                                       EEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAP-----RSP
                                                                                                                                                                                                                                                                                                                                                                          RPRFRELVSEFSRMARDPQRFVVIQNEDLG--PASPLDSTFYRSLLEDD----DMGDLVDA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAVCMSSQMMLITQLMPLGCLLDYVRNNRDKIGSKALLNWSTQIAKGMSYLEEKRLVHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVV--TYICROKOKAKKETVKMTMALSGCEDSEPLRPSNIGANLCKLRIVKDAELRKGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MFNCTSKCPLEMRHVNYQYTAIGPYCAASPPRSSKITANLDVNMIFIITGAVLVPTICIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REQCETECPADHYTDEEQRECFQRHPECNGCTGPGADDCKSCRNFKLFDANETGPYVNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDGNIR ILDQTFSGFQDVYANYTMGPRYIPLDPERREVFSTVKEITGYLNIEGTHPQFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFGSLAFLPESFDG--DPASNTA------PLQPEQLQVFETLEEITGYLYISAWPDSLPD
                                                                          TCQPGPNNNNNMN-----NPNQNNMAAVGVAAGYM---
                                                                                                                TCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAV 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAARNVLVQTPSLVKITDFGLAKLLSSDSNEYKAAGGKMPIKWLALECIRNRVFTSKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGMGAFGRVYKGVWVPEGENVKIPVAIKELLKSTGAESSEEFLREAYIMASEEHVNLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKCPD-GY--FWEYVHPQEQGSLKPLAGRAVCRKCHPLCELCTNYGYHEQVCSKCTHYKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FCVARCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFNGTCIADCGYISNAYK--FDNRTCKICHPECR----TCNGAGADHCQECVHVRDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWPAIQKEPEQKV--WVN----ENLRADLCEKNGTICSDQCNEDGCWGAGTDQCLTCKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SC-----VDLDDKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDLSYMPIWKF -- PDEEGACQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IVSAVVGILLVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SGVK-----
                           ---PPPAFSP-AFDNLYYWD 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CPI-----NCTH---
                                                                                                                                                           -LDLPVDEDDYLMP-
                                                                                                                                                                                                                                              - DEMPKLNRYCKDP
                                                                        DLIGVPVSV
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ERBB_ALV

ID BALV

AC PRO53

AC PRO53

DT 15-JU

DT 15-JU

DT 15-JU

DT 15-JU

DT 15-JU

CC Virus

RA AVian

OX NCBI
RA MEDLI

RA MELL

RA Critt

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PIR; B00643; TVFVLV.
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RASPLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGA
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165
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
Crittenden L.B., Raines M.A., Kung H.-J.;
"C-erbB activation in ALV-induced erythroblastosis: novel
"C-erbB activation in ALV-induced erythroblastosis of
                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS50011; PROTEIN KINASE DOM;
Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00534;
21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino-truncated EGF receptor.";
Cell 41:719-726(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M10066; AAA48763.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase
InterPro; IPR001245; Tyr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPOSINE PHOSPHATE.

TYPOSINE PROPEIN IS PRODUCED BY ERYTHROLEUKEMIA CE MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CE IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VI AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.

MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein
CAHFIDGPHCVKACPAGVLGENDTL-VWKYADANAVCQLCHPNCTRGCKGPGLEGCP---
                                                  CAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQ
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                     Phosphorylation.
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165
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                                                                                                              25.6%;
                                                                                                                                                                                            70891 MW;
                                                                                                  79;
                                                                                             Score 1749.5;
Pred. No. 1.4e
79; Mismatches
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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ATP-binding;
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RESULT 13

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DT 21-JUL
DT 15-JUN
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  SEQUENCE OF 1-152 FROM N.A.
MEDLINE=84223957; PubMed=6328658;
Debuire B., Henry C., Benaissa M., Bi
Saule S., Martin P., Stehelin D.;
"Sequencing the erbA gene of avian er
new type of oncogene.";
Science 224:1456-1459(1984).
-i- CATALYTIC ACTIVITY: ATP + a prote
                                                                                                                                                              SEQUENCE
STRAIN=H;
                                                                                                                            MEDLINE=84026539; PubMed=6313229;
Yamamoto T., Nishida T., Miyajima N., Kaw
"The erbB gene of avian erythroblastosis
                                                                                                                                                                                            Avian erythroblastosis virus (strain ES4).
Viruses; Retroid viruses; Retroviridae; Av
NCBI_TaxID=79685;
                                                                                                                                                                                                                                                  P00535;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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family.";
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Best Local Sim
Matches 360;
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DOMAIN 13
NP BIND 13
BINDING 16
ACT SITE 25
CONFLICT 25
CONFLICT 14
CONFLICT 14
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                                                                          YRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLE
                              ICTIDVYMIMVKCMMIDSECRPRFRELVSEFSRMARDPQRFVVIQ-NEDLGPASPLDSTF
                                                                                                                                                                                                                APNQAHLRILKETEFKKVKVLGSGAFGTIYKGLWIPEGEKVKIPVAIKELREATSPKANK
                                                                                                                                                                                                                             MPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANK
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; pD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1
PROSITE; PS00109; PROTEIN KINASE TYR; 1
PROSITE; PS00101; PROTEIN KINASE DOM; 1
Transferase; Tyrosine-protein kinase; A:
Transferase; Tyrosine-protein kinase; A:
                                                                                                                                                                                                                                                                                                                    EMBL; K02006; AAA42394.1; ALT_INIT.
EMBL; K01216; AAA42400.1; -.
PIR; A00644; TVYUH.
                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN CHICKENS.

MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATE RECEPTOR FOR EPIDERWAL GROWTH FACTOR.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
DISEASE: THE V-ERBS ONCOGENE TRANSFORMS AVIAN
ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS
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ilarity 52.2%;
Conservative 7
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76;
                                                                  PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
R -> W (IN REF. 2).
S -> F (IN REF. 2).
I -> V (IN REF. 2).
  Score 1703; DB 1;
Pred. No. 4.1e-84;
6; Mismatches 128
                                                       -> F (IN REF. 2)
-> V (IN REF. 2)
76EBCDD06745D609
                                                                                                                                                                                ATP-binding;
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                              DB 1;
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    Indels
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  Query Match
Best Local
                                                                     Glycoprotein; I
DOMAIN 133
NP BIND 133
BINDING 166
ACT SITE 25
VARTANT 27
SEQUENCE 540
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Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
"A single amino acid substitution in v-erbB confers a thermolabile phenotype to ts167 avian erythroblastosis virus-transformed erythrocells.";
Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P11273;
01-JUL-1989
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                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS00109; PROTEIN KINASE TYR; PROSITE; PS50011; PROTEIN KINASE DOM;
                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; I.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; Tyrko; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M13179; AAA42401.1; -.
PIR; A25231; TVFVEB.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001245; Tyr_pkinase.
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Viruses; Retroid viruses; Retroviridae; Avi
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transforming protein
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    Local Similarity
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                                                                                                                                                                                                                                     Tyrosine-protein kinase;
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ACTIVITY: ATP + a protein
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Y SIMILARITY).
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                        Length 540;
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01-JAN-1990
15-JUN-2002
Epidermal gro
SEQUENCE FROM N.A.

MEDILINE-88261272; PubMed=3260329;

Lax I., Johnson A., Howk R., Sap J., Bellot F., Winkler Ullrich A., Vennestrom B., Schlessinger J., Givol D.;

"Chicken epidermal growth factor (EGF) receptor: cDNA c expression in mouse cells, and differential binding of transforming growth factor alpha.";

Mol. Cell. Biol. 8:1970-1978(1988).

-i- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDIN
                                                                                                                                                                                                                                                                                                                CHICK
EGFR_CHICK
                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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InterPro; IPR000719; Eux_pkinase.
InterPro; IPR002114; Furin-like.
InterPro; IPR002114; Fur_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complianduction of the tyrosine kinase activity, stimulation of synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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Similarity
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                                                                                                                     OFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNG---SVTCFGPEADQCVACAH
                                                                                                                                                          TMNWRSLFATQS-----QKTKIIQNRNKNDCTADRHVCDPLCSDVGCWGPGPFHCFSCR
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 KTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTLRRLLQERELVEPLTP
                       PLTSIVSAVV-GILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTP
                                                   FIDGPHCVKACPAGVLGENDTL-VWKYADANAVCOLCHPNCTRGCKGPGLEGCP---NGS
                                                                                                       FFSRQKECVKQCNILQGEPREFERDSKCLPCHSECLVQNSTAYNTTCSGPGPDHCMKCAH
                                                                                                                                                                                      TVPWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCS
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Search completed: July 22, 2003, 08:46:40 Job time : 20.2793 secs

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Result
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Q9qx70 rattus norv
Q9ep98 mus musculu
Q9yh40 xiphophorus
Q9w6f6 gallus gall
P79754 fugu rubrip
Q9bih9 anopheles g
Q9uk79 homo sapien
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DT 01-JAN-1998 (TIEMBLrel. 05, Created)

DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update)

DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update)

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DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update)

DE 10-JAN-1998 (TIEMBLrel. 05, Last sequence update)

DC Consisted (Dog).

Canis familiaris (Dog).

CR ENBLYSOLS; Metazoa; Chordata; Craniata; Euteleostomi;

CR Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canidae;

CR MCH TAXID-9615;

RN [1]

TOR SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                    DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT
|||||||||||||:::::
YNYLSTDVGSCTLVCPLNNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MELAALCRWGLLLALLPPGAASTQVCTGTDMXLRLPASPETHLDMLRHLYQGCQVVQGNL
   GDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEAPRSP
                                                                                                 YLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESI
                                                                                                                                                                                                                   IAAVVGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLIDTNRFSACPPCSPACKDAHCWGASSGDCQSLTRTVCAGGCARCKGPQPTDCCHEQC
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Pred. No. 0;
44; Mismatches
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                                                             PAREI
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                                                            POLLEKGERLPOPPICTIDVYMI
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                          R Pfam; PF00069; pkinase; 1.

R Pfam; PF01030; Recep L domain; 2.

R PFINTS; PR00109; TYRKINASE;

R ProDom; PD000001; Euk pkinase; 1.

R SMART; SM00261; FU; 3.

R SMART; SM00219; TYRKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE ATP; 1.

R PROSITE; PS50011; PROTEIN_KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP: 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP: 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP: 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP: 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP: 1.
  Query
Best I
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Q9QX70;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
Epidermal grugger
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                       STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
Petch L.A., Harris J., Raymond V.W.,
                                                                                                                                   InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                   Guttridge K., Dawson T.L., E
Submitted (NOV-1999) to the
EMBL; M37394; AAF14008.1; -.
HSSP; P11362; IFGK.
                                                                                                                                                                                                                         STRAIN-FISHER;
                                                                                                                                                                                                                                                                 Petch L.A
                                                                                                                                                                                                                                                                        SEQUENCE FROM N
STRAIN=FISHER;
                                                                                                                                                                                                                                                                                                      "A truncated, secreted form of the epidermal growth encoded by an alternatively spliced transcript in no Mol. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FISHER; TIS
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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  Local
          Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYL
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                                                                                                                                                                                                                                                       (NOV-1991)
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0 (TrEMBLrel. 13, Last s
12 (TrEMBLrel. 21, Last a
growth factor receptor.
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; TISSUE=LIVER;
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JI.SUE=LIVER;

Dawson T.L., Earp H.S.;

Dawson T.L., Earp H.S.;
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Score 3113;
Pred. No. 6.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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         Length 1209;
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; Murinae; Rat
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                                      kinase
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-P 1127 PE 1235

1084

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Matches
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                                                                                                                       ALESILHRIYTHQSDVWSYG
                                                                                                                                 ALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTI
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                                                                                                                                                                                                                                                                                     AHLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILD
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                                                           GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
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                                                                                                                 VIVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTI
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Q9EP98;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 21, Last sequence upda
01-JUN-2002 (TrEMBLrel. 21, Last annotation up
Epidermal growth factor receptor isoform 1.
EGFR.
EGFR.
Mus musculus (Mouse).
Musmusculs; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep L domain; 2
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1
SMART; SM00261; FU; 5.
SMART; SM00220; S TKC; 1.
SMART; SM00219; TYRKC; 1.
                                                                                                             HSSP; p11362; 1FGK.
MGD; MGI:95294; Egfr.
InterPro; IPR000345; CytC heme_bind.
InterPro; IPR0003494; EGFR_L domain.
InterPro; IPR000719; Euk_bkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                            Submitted (JUN-2000) to the E
EMBL; AF275366; AAG28045.1; -
EMBL; AF275364; AAG28045.1; J
EMBL; AF275365; AAG28045.1; J
EMBL; AF275367; AAG28045.1; J
EMBL; AF275367; AAG24386.1; -
                                                                                                                                                                                                                                                                                                                                                  Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., I
Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland
Balasubramaniam S., Crossley T.O., Magnuson T.R., James
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                              mouse alternative
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aryota; Metazoa; Chordata;
malia; Eutheria; Rodentia;
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E; PS00107; PROTEIN KINASE ATP; 1
E; PS50011; PROTEIN KINASE DOM; 1
E; PS500109; PROTEIN KINASE TYR; 1
nding; Receptor; Transferase.
CE 1210 AA; 134840 MW; 62CD02
LRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMI
                    ASVDNPHVCRLUGICLTSTVQLITQLMPYGCLLDYVREHKDNIGSQYLLNMCVQIAKGMN
                                                       AGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLLNMCMQIAKGMS
                                                                          CVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIV
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ilarity 49.4%;
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DT 01-MAY-1999 (TrEMBLrel.)
DT 01-OCT-2000 (TrEMBLrel.)
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DE RECEPTOR YYOSINE KINAS
GN XMRK.

OS Xiphophorus xiphidium.
OC Eukaryota; Metazoa; Cho
OC Actinopterygii; Neopter
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Interpro; IPR000494; EGFR L domain.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR0002174; Furin-like.
Interpro; IPR001899; Gram_pos_anchor.
Interpro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF001030; Recep_L domain; 2.
PRINTS; PR00109; TYTKINASE.
PRODOM, PD000001; Euk_pkinase; 1.
SMART; SM00210; TyrKc; 1.
SMART; SM00210; TyrKc; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_PROSITE; PS00190; GRAM_POS_ANCHORING; UN STRAIN=RIO PURIFICATION;
MEDILNE=98241172; PubMed==9582016;
Dimitrijevic N., Winkler C., Wellbrock C.,
"Altschmied J., Schartl M.;
"Activation of the Xmrk proto-oncogene of
overexpression and mutational alterations.
Oncogene 16:1681-1690(1998). EMBL; U53471; AAD10500. HSSP; P11362; 1FGK. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus. PURIFICATION; (TrEMBLrel. 10, (TrEMBLrel. 15, (TrEMBLrel. 21, PRELIMINARY; kinase to the 15, Last sequence up 21, Last annotation proto-oncogene. EMBL/GenBank/DDBJ Created) UNKNOWN 1165 UNKNOWN_1. С., ₿ on update) Xiphophorus ."; Gomez databases A : : Neoteleostei à

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PS50011; PROTEIN KINASE DOM; 2.
PS00109; PROTEIN KINASE TYR; 1.
PS00109; PROTEIN KINASE TYR; 1.
ing; Kinase; Transferase; Tyrosine-protein
1165 AA; 129614 MW; 7F7EE38D8771A74E C
                                    NWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGK
                                                                       MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
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         VPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQ
                                                                                                                                                                                                                                                                                    HNTHLCFVHTVPWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGP
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InterPro; IPR002174; FNUTIN-1ike.
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InterPro; IPR001245; Tyr_pkinase.
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InterPro; IPR001049; YLP mocif.
Pfam; PP00757; FUTIN-1ike; 1.
Pfam; PP00759; Purin-1ike; 1.
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Pfam; PP00757; YLP; 7.
PRINTS; PR00109; TYRKINASE.
PRODOM; PP000001; Euk_pkinase; 1.
PROST; SM00219; TYRK; 1.
SMART; SM00219; TYRK; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS000652; TNFR_NGFR_1; UNKNOWN_1.
Kinase; Tyrosine-protein kinase.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Eukaryota; Aves; Neognathae; Galliformes;
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01-NOV-1999
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NON_TER
SEQUENCE
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MEDLINE=99263203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QP-QNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGACQPC
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                                                              CNGTLRKQVATLAKEDSSTORYSADPTVFIPERVIRGELDEDGYMTPMRDKPKTDYLNPV
                                                                                                                                              PPIYTSRTRIDSNRNQFVYRDGGYAAEQGV-PMPYRAPGCIIPEAPVAQGATAEIFEDTC
                                                                                                                                                                                                                                                                                                                                            LMTFGAKPYDGIPAREIPDLLEKGERLPOPPICTIDVYMIMVKCWMIDSECRPRFRELVS
                                                                                                                                                                                                                                                                                                                                                                                                        SPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYRKFTHQSDVWSYGVTIWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELGSGLALIHHNTHLCFVHTVPWDQLFRFNNFTVSFWLRVPKVSA-----SHLEECVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSL
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                                                                                                      GMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPS-----
                                                                                                                                                                                                                                   EFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLVTQLMPHGCLLDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVK
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                                                                                                                                                                                                                                                                                                                     LMTFGGKPYDGIPTREIPDLLEKGERLPOPPICTIDVYMVMVKCWMIDADSRPKFKELAA
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Best Local S
Matches 516
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InterPro; IPRO00719; Euk pkinase.
InterPro; IPRO00719; Furin-like.
InterPro; IPRO012174; Tyr pkinase.
InterPro; IPRO01245; Tyr pkinase.
Pfam; PF000757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00009; Recep L domain; 2.
ProDom; PF000001; Euk pkinase; 1.
SMART; SM00201; FU; 3.
SMART; SM00261; FU; 3.
SMART; SM00261; TYFKG; 1.
KINASE ATP; 1
PROSITE; PS001107; PROTEIN KINASE DOM; 1
PROSITE; PS00111; PROTEIN KINASE DOM; 1
ATP-binding; Transferase.
SEQUENCE 1328 AA; 148613 MW; A33303:
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01-MAY-1997
01-JUN-2002
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P79754;
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EMBL; AF056116; AAC34391.1;
HSSP; P11362; 1FGK.
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Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wnt1 locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rubripes.";
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             AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPT
                                                                                             IQFNGERGVCH---KSC-GNYCWGPGKDQCQILTKTVCAPQCNDRCFGTSPRDCCHIECA
                                                                                                                                                                                                             LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT
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                                                     AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY
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Pfam; PF001030; Recep L domain; 2.
Pfam; PF001030; Recep L domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00261; FU; 7.
SMART; SM00220; S TYC; 1.
SMART; SM00219; TYRC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00119; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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NON TER
SEQUENCE
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"Cloning, expression and localisation of the A epidermal growth factor receptor."; submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL; AJ301655; CAC35008.1; -...
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Putative epidermal growth factor receptor (Fragme
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InterPro; IPRO00494; EGFR L domain.
InterPro; IPRO00719; Euk Dkinase.
InterPro; IPRO02174; Furin-like.
InterPro; IPR002290; Ser thr Dkinase.
InterPro; IPR001245; Tyr_Dkinase.
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Eukaryota; Metazoa; Arthropoda; Tracheata; H
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                                                                                    HNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGITELEFAGCKKIFGSLAFL
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194; Mismatches 386;
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                                                                                                                                                                                                                                                                                                                   VSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLEDDDMGDLV------
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Best Local Sim:
Matches 341;
QBR2X1 PRELIMINARY; PRT; 367 AA.
QBR2X1;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence upda
01-JUN-2002 (TrEMBLrel. 21, Last annotation up
Hypothetical 40.2 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
NCBI_TaxID=10090;
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Submitted (SEP-2000) to the EMBL/Gene
EMBL; AF17761; AAD56009.2; -.
InterPro; IPR000494; EGFR L domain.
InterPro; IPR002174; Furin-Tike.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep L domain; 1.
SMART; SM00261; FU; 1.
SEQUENCE 419 AA; 45472 MW; FECIBE
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Q9UK79;
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MEDLINB-99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A., Adelma
"The HER-2/neu receptor tyrosine kinase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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nilarity 98.8%;
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                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Matches 323
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR004028; Retro M.
Interpro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF02813; Retro M; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
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SEQUENCE FROM N.A.
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SECAUSE R.;
Submitted (APR-2002) to the El
EMBL; BC027080; AAH27080.1; -
Hypothetical protein.
SEQUENCE 367 AA; 40163 MW;
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Underson A., Beug H.;
"Retroviral capture of c-erbB proto-oncogene evolution of distinct viral genomes carrying different transforming capacities.";
Oncogene 9:1307-1320(1994).
EMBL; $69372; AAC60725.1; -.
HSSP; P03322; 1A6S.
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MEDLINE=94203659; PubMed=8152791;
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11950;
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01-NOV-1996 (TrEMBLrel. 01, L
01-MAR-2002 (TrEMBLrel. 20, L
SEQUENCE FROM N.A.

MEDLINE=94203659; PubMed=8152791;

Vennstrom B., Raynoscheck C., Jansson L., Doe
Johnsson A., Beug H.;

"Retroviral capture of c-erbB proto-oncogene
evolution of distinct viral genomes carrying
different transforming capacities.";
                                                                                                            Avian rous-associated virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                            V-erbB protein (Fragment).
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ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 729 AA; 80649 MW; 84D2F6914EFE1D63 CRC64;
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                                                                                                                                                                                                                                                                                            ARPAGATLERAKTLSPGKNGVVKDVF----
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Pred. No. 1.3e-121;
5; Mismatches 118;
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|---SRTPLLSSLSATSNNSATNCID
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                                                    Doederlein
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Best Local S
Matches 357
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InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TYrKC; 1.
SMART; SM00219; TYrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
OBWYVO;

Ol-MAR-2002 (TrEMBLrel. 20, Created)

Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)

Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Hypothetical 44.7 kDa protein.
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EMBL; S69372; AAC60727.1; -
HSSP; P11362; 1FGK.
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Local Similarity 55.4%;
tes 357; Conservative 7;
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                                                                                                                                                                            RYSEDPTVPLPSET--DGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLE
                                                                                                                                                                                                                                                             LPSPTDSKFYRTLMEEEDMEDIVDADEYLVPHQGFF------
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                                                                                                                                           RAKTLS PGKNGVVKDVF----
                                                                                                                                                                   RYSSDPTGNFLEESIDDGFL----
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                                                             PRELIMINARY;
                                                                                                                    -TAMVQNQIYNNISLTAISKLPMDSRYQNSHSTAVDNPEYL
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Pred. No. 1.2e-121;
3; Mismatches 112;
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Best Local Sim
Matches 330;
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SEQUENCE FROM N.A.

Huang Y., Zhou X.M., Zhang P.P., Ji
Wan D.F., Gu J.R.;
Whan D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;
When D.F., Gu J.R.;

Interpro; IPR002048; EF-hand.
Interpro; IPR002048; EF-hand.
Interpro; IPR000719; Euk pkinase.
Interpro; IPR001245; Tyr pkinase.
Interpro; IPR004019; YLP_motif.
Pfam; PP00069; pkinase; I.

Pfam; PP00069; pkinase; I.
                                                                                                      Q64895 PRELIMINARY;
Q64895;
Q64895;
Q1-NOV-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TrEMBLrel. 21, La
Q1-JUN-2002 (TrEMBLrel. 21, La
Gag,v-erb-A,v-erb-B protein.
GAG,V-ERB-A,V-ERB-B.
                              Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11861;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 412 AA; 4
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SMART; SM00219; TyrKc; 1.
FROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM;
UNDERGRADE PS0011; PROTEIN_KINASE_DOM;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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FROM
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                                                                                                                                                                                                                                                                                                                                                            APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFG
                                                                                                                                                                                                                                                                                                                                                                                                       YYWD-QDPPER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAVENPEYLTPQGGAALSPTLLLPSAQPSTTSITGTRTHQSGGLHPAPSKGHLRQRTQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVENPEYLTPQGGAAPQP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYV
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N.A
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Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44702 MW;
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Last sequence tast annoted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1697.5;
Pred. No. 2.8
                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function
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                                                             Avian
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                                                             retroviruses
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Best Local S
Matches 358
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R Probom; PD0000015; Znf C4steroid; 1.

R SMART; SM00439; HOLI; 1.

R SMART; SM00319; TyrKc; 1.

R SMART; SM00309; Znf C4; 1.

R SMART; SM00309; Znf C4; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS001109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS001109; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

W ATP-binding; DNA-binding; Nuclear protein; Receptor; W Transcription regulation; Transferase; Tyrosine-protein kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; pkinase; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR000398; STRDHORMONER.
PRINTS; PR000398; STRDHORMONER.
PRINTS; PR00010; Five Printses.
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SEQUENCE 9
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EMBL; X52211; CAA36459.1; JOINED.
HSSP; P10828; 2NLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90206603; PubMed=1969616;
Bruskin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.
"Six amino acids from the retroviral gene gag greatly enhance th
transforming potential of the oncogene v-erb-B.";
Oncogene 5:15-24(1990).
-i- SUMCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                               762
                                                                                            934
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AREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFV 993
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                                                          ASEISSVLEKGERLPOPPICTIDVYMIMVKCWMSGADSRPKFRELIAEFSKWARDPPRYL
                                                                                                                      KQLGADEKEYHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIP
                                                                                                                                    RLLDIDETEYHADGGKVPIKWMALESILRRRFTHOSDVWSYGVTVWELMTFGAKDYDGIP
                                                                                                                                                                                                                                         IPVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPYGCLL
                                                                                                                                                                                                                                                          IPVAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTOLMPYGCLL
                                                                                                                                                                                                                                                                                                                      RRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVK
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                                                                                                                                                                                                                                                                                                      RRILGERELVEPLTPSGEAPNOAHLRILKETEPKKVKVLGFGAFGTVYKGLWIPEGEKVT
                                                                                                                                                                                                                                                                                                                                                                NCTRGCKGPGLEGCP---NGSKTPSIAAGVVGGLLCLVVVGLGIGLYLRRR-HIVRKRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%;
51.7%;
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Pred. No. 2.1e
73; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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Best Local S
Matches 345
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Scotting P., Vennstrom B., Jansen M., Gr
"Common site of mutation in the erbB gen
virus mutants that are temperature sensi
Oncogene Res. 1:265-278(1987).
EMBL; X06943; CAA30024.1; -.
HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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01-NOV-1996
01-NOV-1996
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ProDom; PD000001; Euk pkinase; 1.

SMART; SMO0219; TYPKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Transferase; Tyrosine-protein
SEQUENCE 545 AA; 60899 MW; 140DCE8CCAOF
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Avian Erythroblastosis virus (Te34) v-erbB gene.
Avian erythroblastosis virus.
Viruses; Retroid viruses; Retroviridae; Avian type
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                                                                                                                      LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETE
                                                                                                                                                                                             YHADGGKVPIKWMALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLE
                                                                                                                                                                                                                                                                                        VEPLTPSGEAPNQAHLRILKETEFKKVKVLGFGAFGTVYKGLWIPEGEKVTIPVAIKELR
                                                                                                                                                                                                                                                                                                                    VEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLR
YHAEGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP--DHCMKCAHFIDGPHCVKACPAGVLGENDTL-VMKYADANAVCQLCHPNCTRGCKGP
                                                                                           IGSQYLLNWCVQIAKGMNYLEERHLVHRDLAARNVLVKTPQDVKITDFGLAKQLGADEKE
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Pred. No. 4e-1
70; Mismatches
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C STRAIN-C37BL/G; TISSUE-LIVER;

K MEDLINE-21085660; PubMed-11217851;

K MEDLINE-21085660; PubMed-11217851;

K Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito T., Osazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosaavant T.,

CA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

CA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

CA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

CA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

CA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

CA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

CA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

CA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

CA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

CA Blake J., Boffelli D., Hofmann M., Carninci P., de Bonaldo M.F.,

CA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

CA H., Matsuo P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

CA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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01-NOV-1999 (TrEMBLrel. 12
01-NOV-1999 (TrEMBLrel. 12
01-JUN-2002 (TrEMBLrel. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell
Lampland A.L., Balasubramaniam S., Crossley T.O., Mag
Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Sinclair A.S., Crossley T.O., Magnuson T.R., James C.D.,
Maihan M.T., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Alternative Transcripts from the Human and Mouse EGFR Carboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse alternative
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Mammalia; Eutheria;
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Egfr transcripts and
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Rodentia;
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12, Last sequence update)
21, Last annotation update)
: receptor (Epidermal growth
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-SRTPLLSSLSATSNNSATNCIDRNGG:
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Sciurognathi; Muridae;
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; Murinae; Mus
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Matches 283
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Hayashizaki Y.;
"Functional annotation of a f
Nature 409:685-690(2001).
EMBL; AR275366; AAG280447.1; J
EMBL; AR275364; AAG28047.1; J
EMBL; AR275364; AAG28047.1; J
EMBL; AR275364; AAG28047.1; J
EMBL; AR004944; BAB23688.1; -
EMBL; AK004911; BAB23684.1; -
EMBL; AK004911; BAB23662.1; -
MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki H., Sato K., Schoenbach C.,
Suzuki H., Toyo-oka K., Wang K.H.,
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InterPro; IPR002174; Furin-Tike.
                                               531
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CVKTCPAGIMGENNTL-VWKYADANNVCHLCHANCTYGCAGPGLQGC
                                                        RGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPF
                                                                                                                                    HAFENLEIIRGRTKQHGQFSLAVVGLNITSLGLRSLKEISDGDVIISGNRNLCYANTINW
                                                                                                                                              HEKYCTAISGDLHILEVAFKGDSETRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDL
                                                                                                                                                                                           -FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDL
                                                                                                                                                                                                                                          LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                            RGRECVEKCNILEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPH
                                                                                                            DQLFRFNNFTVSFWLRVPKVSASHLE-ECVGEGLACHQLCARGHCWGPGPTQCVNCSQFL
                                                                                                                                                                                                                          VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFK-DTLSINATNIK
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ilarity 43.7%;
Conservative 99
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Pred. No. 3.8
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Weitz C.,
egawa Y., Ka
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Whittaker
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ker C., Wilming
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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6842
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4403.399 Million cell updates/sec
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                     AAY92620
AAE12130
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AAW01111
AAW92406
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AAY84780
AAB85458
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Human heregulin 2
Human tyrosine kin
HER2 transgene pla
Human HER2 (ErbB2)
HER-2/neu protein.
Human HER-2/neu on
Human HER-2/neu pr
Amino acid sequenc
Human HER-2/neu pr
HER2/neu amino aci
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3077	3083	3083	3084	3084	3116	3118	3118	3118	3118	3242	3345	3410	3410	3448	3448	3450	3596	3596	3975.5	10	4712	4712	5825.5	5825.5	~	~	m	6309	6	58	62	62	6626	62	
45.0	45.1	5	5	5	45.5	5	5	5	5	47.4	8	9.	9.		50.4			<u>ب</u>	58.1	8	8.	8	•	85.1	5	<u>ب</u>	5	2	94.4		٠,	٥.	96.8		
1210	600	589	587	583	1210	1210	1210	1210	1210	624	951	645	645	653	653	782	712	712	926	920	919	919	1256	1256	1256	1256	1256	1200	1223	w	1255	25	1255	25	
23	23	23	23	23	22	23	23	21	21	H	21	22	22	23	21	18	23	21	23	23	23	21	23	22	21	23	21	21	23	14	23	23	23	23	
ABP51768	AAE20482	AAE20484	AAE20481	AAE20483	AAB68420	9	301	AAY50616	AAB19259	AAR08222	499	AAB61593	AAB60408	AAM51145	AAB21200	AAW19764	AAM51149	AAB21204	AAM51153	AAM51152	1	AAB21203	AAM51151	AAG62860	AAB21206	114	119	120	892	AAR39568	711	AAM51143		AAE24067	
ø	protein	protein	prot	prote	acid seque	epidermal g	Her-1 prote	EGF r	acid sec	cellular po	Fv-erbB	ErbB2	ErbB2 onc	'n	cellula	-GM-CSF immun	/neu extrac	HER-2/neu	e Her-2/neu	e Her-2/neu e	/neu extrac	HER-2/neu	Her-2	acid seque	se Her-2/ne	Her-2/neu	ER-2/neu pr	HER-2/n	east ca	nce of c-er	Her-2/neu	r-2/neu	TO.	Human Her-2 protei	

ALIGNMENTS

RESULT 1 AAY92620 ID AAYS

AAY92620 standard; Protein; 1255 AA

Human heregulin 2 (Her2).

10-AUG-2000 AAY92620;

(first entry)

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Region
                                                                                                                                                                 Key
Domain
                                                                                                                                                                                                                    self-protein; cancer; breast cancer; prostate car
cell-associated peptide antigen; foreign epitope.
 Domain
                                Region
                                                                                                  Region
                                                                                                                                 Region
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                Heregulin 2; Her2; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer;
/label= insertion region
/note= "suitable for foreign epitope insertion"
174..323
                                /label= insertion region
/note= "suitable for foreign
149..163
                                                                                                        /label= insertion_region
/note= "suitable for foreign epitope insertion"
                                                                                                                                           /note= "mature polypeptide"
                                                                  103..117
                                                                         /label= insertion_region
/note= "suitable for foreign
                                                                                                                                                       /label= N-terminal
                                                                                                                                                                           ocation/Qualifiers
                                         epitope insertion"
                                                                          epitope insertion'
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This is the human heregulin 2 (Her2) sequence. Immunogenic analogue, Her2 can be used in the claimed method as an autovaccine to induce a response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign helper epitopes were identified (see features table). The method
                                                                               Inducing peptide a
                                                                                                                                         Steinaa L,
                                                                                                         N-PSDB;
                                                                                                                                 Gautam
                                                                                                                                                                            05-OCT-1998;
20-OCT-1998;
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antigens for the t
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Birk P, Karlsson
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98US-0105011
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/note= "suitable For foreign
624..654
/label= Transmembrane_domain
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/note= "suitable
655..1010
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210..224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (PGP8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respectip PA and including at least one foreign T helper epitope are also claimed The method is used to treat prostate, prostate/breast or breast cancer when the DA is human PSM.
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                                     VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                      VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
                                                                                                                                                                                                                                                                                                DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
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LKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDEAYVM
                                                                                                                                                                            LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                                                                                                                                                                      PWDQLFRFNNFTVSFWLRVPKVSASHLEECVGBGLACHQLCARGHCWGPGPTQCVNCSQF
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                                                                                                                                                           LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therapeutic compound; major histocompatibility complex; vaccine; antigenic peptide; MHC; immunoregulatory; immune response; HER-2; adoptive immunetherapy; anti-cancer; breast cancer antigen; APC; antigen presenting cell; human; tyrosine kinase-type receptor.
                                                                                                Nicolette
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Novel synthetic therapeutic compound for inducing immune response for use in adoptive immunotherapy, has enhanced binding to major histocompatibility molecules and enhanced immunoregulatory propert nanced binding to major immunoregulatory properties

Claim 4 Page 63-67; 69pp; English

peptides) with enhanced binding to major histocompatibility complex (MHC) molecules and enhanced immunoregulatory properties relative to their natural counterparts. Compounds of the invention are useful communoregulatory properties relative to their natural counterparts. Compounds of the invention are useful communorherapy. They are useful as components of anti-cancer vaccines immunorherapy. They are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterised by expression of the breast cancer antigen, HER-2. Compuncleotides that encode peptides of the invention are useful as hybridisation probes and as primers for the detection of genes of gene transcripts that are expressed in antigen presenting cells (APCs), to confirm transduction of polymucleotides into host cells. The present gequence is human tyrosine kinase-type receptor, HER-2. Compounds of the invention are designed based on the HER-2 antigenic peptide (774 - 782).

Sequence 1255 ξ

Query Match
Best Local Similarity
Matches 1226; Conserv

Conservative

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21; 22;

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Score 6632; DI Pred. No. 0; 8; Mismatches

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Erickson
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                                                                                 04-JAN-2001
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                                                                                                                    Homo sapiens
Synthetic.
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2000US-0189844.
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WPI; 200 N-PSDB; 2001-061962/07. DB; AAF24297.

Treating tumors, particularly breast cancers, receptor and does not respond to an anti-ErbB conjugating the antibody to a maytansinoid which overexpress an antibody, comprises

Example 3; Fig 4; 92pp; English.

The present invention provides a method of treating cancer by administering a conjugate of anti-ErbB antibody with a maytansinoid. particular, the antibody is directed against ErbB2 (also known as HER and pl85neu). The method is particularly useful in the treatment of breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, colorectal, thyroid, pancreatic, prostate and bladder cancers. HER2

Sequence 1255 AA;

Query Match Best Local S Matches 1226

Similarity

96.9**%**; 97.2**%**;

Score 6632; D Pred. No. 0; 8; Mismatches

B

Length Indels

1226;

Conservative

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Gaps

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                                  VSAVVGILLVVVLGVVFGILIKRRQQXIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI
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                                                                                    FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HER2; ErbB; epidermal growth factor receptor; receptor; anti-ErbB antibody-maytansinoid conjugate; cancer; tumour; breast; ova: stomach; endometrium; salivary gland; lung; kidney; colon; colorectum; thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder; thyroid; pancreas; prostate; bladder; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder;
                                                                                                                                16-MAR-2000;
05-OCT-2000;
                           (ERIC/)
(SCHW/)
(SLIW/)
                                                                                                                                                                                                            16-MAR-2001;
                                                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenic disorder;
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Example 3; Fig 7; 93pp;
                                                                                                                         anti-ErbB
                                                                                                                                                   N-PSDB;
                                                                                                                                                                      Erickson
                                                                                                                                                   2002-163686/21.
DB; ABK14058.
                                                                                                                               g tumour characterised by overexpression of epidermal receptor, ErbB or cancer in mammal, comprises administ
                                                                                                                                                                      'n
                                                                                                                        antibody-maytansinoid
                                                                                                                                                                     Schwall
                                                                                                                                                                     ø
                                                                                                            English.
                                                                                                                                                                      Sliwkowski
                                                                                                                       conjugate to the mammal
                                                                                                                               administering
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growth

The invention relates to treating a tumour in a mammal, where the tumour is characterised by the overexpression of an epidermal growth factor receptor (ErbB) and does not respond or responds poorly, to treatment with an anti-ErbB antibody, comprising administering to the mammal an anti-ErbB antibody-maytansinoid conjugate. The method is useful for treating cancer or tumours of the breast ovary, stomach, endometrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunological disorders. This sequence represents the human HER2 (ErbB2) polypeptide of the invention.

Sequence 1255 ₽,

Query Match Best Local S Matches 1226

cal Similarity 1226; Conserv

Conservative

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Indels Length

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                                      LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                          PWDQLFRNPHQALLHTANRPE-----DECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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        LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
                                                                                 PWDQLFRNPHQALLHTANRPE-----DECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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96US-0625101
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17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
                       This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
Sequence
                                                                                                                                    Claim
                                                                                                                                                            preventing
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93US-0033644.
93US-0106112.
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{\rm HER} \cdot 2/{\rm neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and prostate cancers -
                                                                                          Claim
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(SMIK ) SMITHKLINE
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The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias. is a member of

Sequence 1255 AA;

Query Match Best Local :

Similarity

96.8**%**; 97.1**%**;

Score Pred.

6626; No. 0;

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                           02-OCT-1998;
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protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                  Claim 3;
                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding erbB-2, inhibitors of
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DB; AAA14812.
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                                                                                                                                                                                                                                                  sequence represents a SPLICE an in-frame deletion of 16 am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel PM
                                                                                                                                                                                                                                                                                                                                                     an erbB 2 receptor protein designated SPLICE the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                English.
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1255 AA;

Similarity

96.8**%**; 97.1**%**;

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                                          LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP
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FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI
                                                                                                                                             DLSVFONLOVIRGRILHNGAYSLTLOGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
                                                                                                                                                                                                       IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
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                                                                                                                  (first
                                                                                  cytostatic;
                                                                                 cell; immunogenic; immune
cytostatic; vaccine; p185;
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New antigen-presenting cells, useful as vaccines for eliciting enhancing an immune response to HER-2/neu protein, particularly for treating or preventing cancer, e.g. breast cancer Cheever MA, 2001-476112/51 Hand-Zimmermann

or y useful

Claim <u>ې</u> Page 41-46; 49pp; English

The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2). 'n

1255 AA;

BG

22;

Length

Query Match
Best Local Similarity 97.1
Matches 1224; Conservative 595 601 535 661 541 481 481 421 421 361 361 301 301 241 241 181 181 121 121 61 61 μ MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL VSAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRI FCVARCPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSI LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP DLSVFQNLQVIRGRILHNGAYSLTLQGIGISWLGLRSLRELGSGLALIHHNTHLCFVHTV PWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCSQF DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLA LRGQECVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPP PWDQLFRNPHQALLHTANRPE-----DECVGEGLACHQLCARGHCWGPGPTQCVNCSQF MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 96.8%; 97.1%; Score 6626; DE Pred. No. 0; 9; Mismatches 22; 6 Gaps 654 600 180 720 594 534 480 480 420 420 360 360 300 300 240 240 180 120 120 60 60

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AAG88 267
ID AAG88
XX AAG88
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                                              Fikes J,
Keogh E;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; HER2/neu; epitope; himmune response; vaccine; tumour-associated antigen;
  WPI; 2001-374995/39
                                                                                                                                                                                 10-DEC-1999;
                                                                                                                                                                                                                                  11-DEC-2000; 2000WO-US33591
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                                                                                                                                                                                 9905-0458299
                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope; human leukocyte antigen; HLA; T cell;
vaccine; tumour; cancer; cytostatic; immunostimulant;
d antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
                                                                              Sidney J,
                                                                            Southwood S,
                                                                         Chesnut R,
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An isolated prepared HER2/new epitope useful in a vaccine for cellular immune responses for the prevention and treatment of English cinducing cancer -

The present invention describes isolated prepared HER2/neu epitopes (I). CC Also described are: (I) a clonal cytoroxic T lymphocyte (CTL) that is CC culture in vitro and binds to a complex of an epitope (I), bound to a CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) CC and a second epitope and the peptide is less than 50 contiguous amino CC acids that have 100% identity with a native peptide sequence of HER2/neu; (CI) and (SI) an isolated nucleic acid encoding a peptide comprising (I) excipient; (4) an isolated nucleic acid encoding a peptide comprising (CI); and (SI) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (II) are useful for comprising (CI) and (III) are useful for inducing cellular immune responses for the detecting the presence of bound T lymphocyte to a tumour associated antigen when incubated with a T lymphocyte to (I) or (II). Epitope chased vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to combine immune response to multiple tumour associated molecules and focus an immune response to multiple tumour associated molecules addressing the problem of tumour variability and reducing the likelihood of tumour variability and reducing the likelihood of tumour easape due to the exemplification of the present invention.

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Query Match Best Local (

Similarity

96.8%; 97.1%;

Score 6626; Pred. No. 0;

B 22;

Length 1255;

S 밁 S 밁 Ś 片 र् 밁 Ś 문 8 밁 S Matches 481 361 361 421 421 301 301 241 241 181 181 121 121 61 61 PWDQLFRENNETVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCSQF DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV ELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAMPDSLP AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP LTLIDTURSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC DPLANTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN Conservative Mismatches 22; Indels 9 Gaps 540 480 420 360 180 480 420 300 240 180 360 300 120 60 240 60

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RESULT 11
AAE24067
ID AAE22
AC AAE24
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                                                            Human; Her-2; epidermal growth factor receptor 2; infection; cance hyperproliferative disorder; prophylaxis; inflammation; antisense; tumour; gene therapy; phosphorothioate backbone.
            WO200222636-A1
                                    Homc. sapiens.
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Novel antisense oligonucleotide which modulates the Epidermal Growth Factor receptor, Her2, is useful for inflammation or to prevent infection in humans he expression for treating of Human

Example 13; Page 95-107; 116pp; English.

The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative disorders e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is human

Sequence 1255 AA;

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                                     PWDQLFRFNNFTVSFWLRVPKVSASHLEECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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                                                                                                                                                               YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT ||||||||||||||:::::
YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
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                      PWDQLFRNPHQALLHTANRPE-----DECVGEGLACHQLCARGHCWGPGPTQCVNCSQF
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The invention relates to an isolated Her-2/Neu polypeptide composition CC effective for eliciting an immune response. The invention is useful for CC eliciting an immune response in a patient, where the patient is human CC leukocyte antigen (HLA)-844 positive or is affected with breast cancer. CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine CC and other compositions for the diagnosis, prevention and treatment of the compositions for the diagnosis, prevention and treatment of CC human malignancies, for stimulating and/or expanding T cells specific for CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a CC patient. The invention is useful for stimulating a T cell response in a CC human patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full CC polypeptide in appropriate host cells. The composition is useful in CC prophylactic or therapeutic applications and for the treatment of cancer, CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-creations. The invention is useful in gene therapy. The
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28-SEP-2000; 2000US-236428P
21-FEB-2001; 2001US-270520P
present sequence is human Her-2/neu protein.
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Mcneill PD, Vedvick
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uery Match 96.8%; Score 6626; DB 23; Length 1255; lest Local Similarity 97.1%; Pred. No. 0; latches 1224; Conservative 9; Mismatches 22; Indels 6; Gaps

1255 AA;

ELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMQYIKANSKFIGIT AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFBSMPNPEGRYTFGASCVTACP DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNDEGRYTFGASCVTACP LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA ELTYLPTNASLSFLODIQEVQGYVLIAHNOVRQVPLQRLRIVRGTQLFEDNYALAVLDNG ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL PMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 300 180 360 360 240 240 180 120 120 60

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          Human Her-2/neu oncogene-encoded p185 glycoprotein.
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Query Match
Best Local Similarity
Matches 1224; Conserv

Conservative

9;

22; 23;

Indels Length

6

Gaps

60 60 96.8**%**; 97.1**%**;

Score 6626; I Pred. No. 0; 9; Mismatches

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Sequence

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The present sequence is that of human Her-2/neu (p185 glycoprotein CC or c-erb87), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu igene is amplified and p185 is overexpressed CC in a variety of cancers, including breast, ovarian, colon, lung and CC prostate cancer. Her-2/neu is a member of the tyrosine kinase CC family of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal CC intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and CC overexpression correlates with a poor prognosis in breast and CC overexpression correlates with a poor prognosis in breast and CC overexpression mucleic acids encoding them, viral vectors, and vaccines CC comprising the fusion proteins or nucleic acid molecules. In CC preferred fusion proteins or nucleic acid molecules. In CC protein is fused to a Her-2/neu intracellular domain or CC protein is fused to a Her-2/neu intracellular domain or CC protein is fused to a Her-2/neu intracellular domain or CC protein is the fusion protein in the form of a vaccine, or by CC transfecting cells of an animal ex vivo with a nucleic acid cells co the animal. The fusion proteins, nucleic acids, and isolated CC encoding the fusion protein, and delivering the transfected cells co the animal. The fusion proteins, nucleic acids, and isolated CC ancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu CC order to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation domain
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                                           LAPSEGAGSDVFDGDLGMGAAKGLQSLFTHDPSPLQRYSEDFTVPLPSETDGYVAFLTCS
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                                                                                                                        The invention relates to a method for inhibiting development of haematological malignancy in a patient by administering a polypeptide comprising an immunogenic portion of Her-2/neu or a polynucleotide encoding the polypeptide. Antigen presenting cells that express the protein can also be administered. The sequences are used for inhibiting development of haematological malignancy such as acute myelogenous leukaemia (AML), chronic myelogenous leukaemia (CML), mDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's lymphoma. This sequence represents the human Her-2/neu polypeptide.
                                                                                                                                                                                                                                                          Disclosure; Page 71-74; 74pp; English.
                                                                                                                                                                                                                                                                                    Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Her-2/neu; cytostatic; haematological malignancy; CML; acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; Hodgkin's lymphoma;
                                                                                                       Sequence
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28-SEP-2000;
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             MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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	QDPPERGAPPSTF OPPERGAPPSTF	ATLERAKTLSPGH ATLERPKTLSPGH	SPLQRYSEDE SPLQRYSEDE	HRHRSSSTRSGGGDLTLGI 	DPQRFVVIQNEDLGPA	GIPAREIPDLLE GIPAREIPDLLE	GLARLLDIDETEYHAI 	GCLLDHVRENRGRLG	PDGENVKI PVAI KVLRI 	IRKYTMRRLLQETEL)	CQPCPINCTHSCVD	CHPECQPQNGSVTC	CVGEGLACHQLCAR CVGEGLACHQLCAR	SWLGLRSLRELG SWLGLRSLRELG		CEKCSKPCARVCYC	PALVTYNTDTFESM
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	DVP 12	VENP 12	LTCS 11	PRSP 10	DDDM 10	DVYMI 96	ESI 9	AKGMS 84	AYVM 78 AYVM 77	QMRI 72 QMRI 71	PLTSI 66	 KDPP 59	CSQF 54 	FVHTV 48	DSLP 42	J. G.	TACP 30

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ALIGNMENTS

A;Reference number: 157622; MUID:87286: A;Accession: 157622 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <TAL> A;Molecule type: mRNA
A;Residues: 1-517, 'RALL', 522,'S', 524-654,'V', 656-1169,'A', 1171-1255 <COU2>
A;Cross-references: GB:M1730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: IS9509; MUID:85272597; PMID:2992089 A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcription:
A;Reference number: 157622; MUID:87286898; PMID:3039351 A;Molecule type: mRNA
A;Residues: 1-1255 <74M>
A;Residues: 1-1255 <74M>
A;COSE-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;COSE-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-exbB-related protooncogene, C-exbB-2, is distinct from the c-exbB-1/epide: A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491; MUID:86016729; PMID:2995967 A;Status: translated from A;Molecule type: DNA A;Residues: 832-909 <REX> A;Molecule type: DNA A;Residues: 740-910 <COUI> A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; A;Reference number: A24571; MUID:86118663; PMID:3003577
A;Reference number: A24571 R; Yamamoto, T.; Ikawa, Nature 319, 230-234, 19 A; Title: Similarity of C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 R;COUSSENS, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, Science 230, 1132-1139, 1985
A;Tille: Tyrosine kinase receptor with extensive homology to A;Reference number: A44188; MUID:86070181; PMID:2999974 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erl A; Accession: I59509 A; Accession: A44188 A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A;Molecule type: DNA A;Residues: 737-1031 <SEM> a, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, 1986 GB/EMBL/DDBJ PID:g183989 EGF receptor shares chromo PID:g553282 A.; McGrath, J.; Seeburg, 1

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A;Cross-references: GB:M16792; NID:g183983; PI
C;Comment: Amplification and overexpression of
C;Genetics:
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A;Genetics: GDB:120613; OMIM:164870
A;Map position: 17921.1-17921.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation o
C;Superfamily: epidermal growth factor recepto
C;Keywords: ATP; autophosphorylation; duplicat
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F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;22-653/Domain: EGF receptor extracellular domain repeat <EE1>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE2>
F;395-605/Domain: transmembrane #status predicted <TMM>
F;395-605/Domain: intracellular medicted <TMM>
F;654-675/Domain: intracellular #status predicted <INT>
F;718-983/Domain: protein kinase homology <KIN>
F;718-983/Domain: protein kinase ATP-binding motif
F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1225;
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       PFNNFTVSFWLRVPKVSASHLE---
                                                                                                                                                                                                                                                                                   DLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTV
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                                                                                                    VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                                               PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
                                                                                                                                                                                                                                                                                                                                                        IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                                                                         VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
                                                                                                                                                                    PWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQEC
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96.8%;
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Pred. No. 2.6e-267;
-PDEEGACQPCPINCTHSCVDLDDKGCPAEQRASP
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                                          LDVPV
                                                                                                VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                                                                                                                                                LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA
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A; Note: C; Geneti A; Gene: A;Molecule type: mRNA
A;Rosidues: 1-1260 <BAR>
A;Rosidues: 1-1260 <BAR>
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A;Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith
Carcinogenesis 12, 1975-1978, 1991
A,7fitle: Direct DNA sequencing of the rat neu oncogene transmembrane doma
2-thiazolyl]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Accession: A61204
A;Status: preliminary
A;Status: preliminary A;Molecule type: DNA
A;Residues: 637-663,'V',665-702
A;Note: authors translated the c RESULT 2
TVRTNU
TVRTNU
protein-tyrosine kinase (EC 2.7.1.112) neu precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #t
C;Accession: A24562; A61204 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-330, 1986
A;Title: The neu oncogene encodes an epidermal growth factor
A;Reference number: A24562; MUID:86118662; PMID:3945311 A; Accession: A24562 Genetics: codon GCA CA for residue #text_change 25 86 Val receptor-related 11-Jun-1999 Smith, domain

R.A.;

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protein.

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C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprote F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>F;658-680/Domain: transmembrane #status predicted <TMN>F;659-680/Domain: protein kinase homology <KIN>F;723-988/Domain: protein kinase ATP-binding motif F;731-739/Region: protein kinase ATP-binding motif F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status F;691/Binding site: phosphate (Thr) (covalent) #status predicted F;758/Active site: Lys #status predicted F;758/Active site: Lys #status predicted
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                                    DEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHRGRLGSQDLLNWCVQ
                                                          DEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQ
                                                                                                                                                                   SPVTFIIATVEGVLLFLILVVVVVGILIKRRRQKIRKYTMRRLLQETELVEPLTPSGAMPN
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     IAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEYHADGGKVPIKW
                                                                                                                                                                                                                                                                                                    ECVEECRVWKGLPREYVSDKRCLPCHPECQPQNSSETCFGSEADQCAACAHYKDSSSCVA
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                                                                                                                                                                                                                                                                                                                                                                                        VPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHCWGPGPTOCVNCSQFLRGQ
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85.3%;
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                                                                                                                                                                                                                                                                                                                          A;Gene: neu
C;Superfamily: epid
C;Keywords: ATP
F;718-983/Domain: p
F;726-734/Region: p
                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p-185 precursor - golden hamster
c;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-19
C;Accession: I48161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Naga
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A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu
A;Reference number: I48161; MUID:94193007; PMID:7908275
A;Accession: I48161
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I48161
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C;Genetics:
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Matches 1075;
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                      LTLIDTNRSRACHPCSPMCKGSRCWGBSSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                             DPLANTTEVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLA
                                                                                                                                                                                                              MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
PVDIDTNRSRACPPCAPACKDNHCWGASPEDCQTLTGTIAPRAVPAARARLPTDCCHEQC
                                                                                                                                              ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                           ELTYLPANATLSFLQDIQEVQGYMLIAHSQVRHVPLQRLRIVRGTQLFEDKYALAVLDNR
                                                                                                                                                                                           MELAAMCGWGLLLALLSPGASGTQVCTGTDMKLRLPASPETHLDIVRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEY 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEE
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                                                                                                                                                                                                                                                                                                                                                                              epidermal
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55, 1994
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                                                                                                                                                                                                                                                                                                                            protein kinase homology <KIN>
protein kinase ATP-binding mov
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                                                                                                                                                                      LTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGA 1196
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                                                                                                                                                                                                                                                 PRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAP 1136
                                                                                                                                                                                                                                                                                                       DDDMGDLVDAEEYLVPQQGFFFPDPAPGAGSTAHRRHRSSSTRSGGGELTLGMEPSGEEP
                                                                                                                                                                                                                                                                                                                         DDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTRSGGGDLTLGLEPSEEEA 1076
                                                                                                                                                                                                                                                                                                                                                                               VYMIMVKCWMIDSECRPRFRELVSEFSRWARDPQRFVVIQNEDLGPSSPLDSTFYRSLLE
                                                                                                                                                                                                                                                                                                                                                                                                       VYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDSTFYRSLLE 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCMQIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLRENTSPKANKEILDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLP
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LDVPV
                                    LDVPV 1261
                                                                                                VENPEYLTPQGGAAPQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLG
                                                                                                                                                LACSPOPEYVNOPEVRPOPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFTFGGA
                                                                                                                                                                                                                        PRSPLAPSEGAGSDVFEGELGMGATKGPOSISPRDLSPLORYSEDPTLPLPTETDGYVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWDQLFRNPHQALLHSGNPSEEECGLKDFACYPLCAHGHCWGPGPTQCVNCSHFLRGQEC
                                                                        VENPEYLVPRGGSASOPH-PPALCPAFONLYYWDODPSERGSPPNTFEGTPTAENPEYLG
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A;Molecule type: mENA
A;Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S',
A;Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S',
', '98-799, 'TD', 802-811, 'R', 813-942 <XUY>
A;Experimental source: A431 human carcinoma cells, which have large
R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Ev
Science 224, 843-848, 1984
A;Title: Expression cloning of human EGF receptor complementary DNA
A;Title: Expression cloning of human EGF receptor complementary DNA
A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615
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GQHUE
GQHUE
epidermal growth factor receptor precursor - human
epidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15:Nov-1984 #sequence revision 27-Nov-1985 #text change 11-Jun-1999
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; F
R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.;
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A; Residues: 1-29 < HALY
A; Residues: 1-29 < HALY
A; Cross-references: GBL*M38425; NID:g181977; PIDN:AAA63171.
A; Experimental source: carcinoma cell line A431-7
A; Experimental source: carcinoma cell line A431-7
R; Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson,
Nature 309, 806-810, 1984
A; Title: Human epidermal growth factor receptor cDNA is hc
A; Reference number: A00642; MUID:84245835; PMID:6330563
A; Accession: A00642
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A; Residues: 1-29 kHA2;
A; Cross references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1;
A; Cross references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1;
A; Haley, J.D.; Waterfield, M.D.
Biol. Chem. 266, 1746-1753, 1991
A; Title: Contributory effects of de Novo transcription and pre A; Reference number: A38672; MUID:91107677; PMID:1988448
A; Accession: A38672
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A;Residues: 1-1210 <UUL>
A;Residues: 1-1210 <UUL>
A;Residues: 1-1210 <UUL>
A;Residues: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
R;IShii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the huma
A;Reference number: A25772; MUID:85270438; PMID:2991899
A;Accession: A25772
              A;Accession: A052
A;Molecule type:
A;Residues: 25-30
                                                                              R; Weber, W.; Gill, G.N.; Speißs, J. Science 224, 294-297, 1984
A; Reference number: A05281; MUID:84172183;
A; Accession: A05281
                                                                                                                                                                                                             A;Experimental source: epidermoid carcinoma cell line A4 R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
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A; Residues: 713-964 <LIN>
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A; Residues: 1-29 <ISH>
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R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros J. Biol. Chem. 260, 5205-5208, 1985 A;Title: Identification of residues in the nu A;Reference number: A60143; MUID:85182650; PM A;Accession: A60143 MUID:85182650; PM A;Accession: A60143 A;Molecule type: protein A;Residues: 740-744, 'X', 746-747 <RUS> R;Mroczkowski, B.; Mosig, G.; Cohen, S. Nature 309, 270-273, 1984
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A;Title: The mouse waved-2 ph A;Reference number: A53183; M A;Accession: A53183 A;Molecule type: mRNA A;Fesidues: 1-1210 <LUE> A;Cross-references: GB:U03425 epidermal growth factor receptor precursor - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 18-Jun-1999 C;Accession: A53183; A43818; S24942; A28941; S45225; 149643 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Je: Genes Dev. 8, 399-413, 1994 GB:U03425 phenotype results from a point; MUID:94170986; PMID:8125255 mutation H.S.; Jenkins, ä

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A;Title: Comparison of EGF receptor sequences as a guide to study the lic A;Reference number: A43818; MUID:91232886; PMID:2030916
A;Reference number: A43818
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A;Accession: A43818
A;Cross-references: GB:X59698
R;Eisinger, D.P.; Serrero, G.
Submitted to the EMBL Data Library, June 1992
A;Reference number: $24942
A;Molecule type: mRNA
A;Residues: 969-971; K', 973-1115, 'D' <EIS>
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A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
A;Reference number: S45325
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphopro
F;1-24/Domain: signal sequence #status predicted <SIG>
F;648-670/Domain: transmembrane #status predicted <TMM>
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A; Residues: 1-971, 'K', 973-1210 < VER>
A; Residues: 1-971, 'K', 973-1210 < VER>
A; Cross references: EMBL:X78987; NID:9488830; PIDN:CAA55587.
A; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59; 193
A; Title: Expression of the epidermal growth factor receptor
A; Reference number: 149643; MUID:93126380; PMID:7678348
A; Accession: 149643
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F;720-728/Region: protein kinase ATP-binding motif
F;720-728/Region: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
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A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
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                                                                                                                                                      YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN------
                                                                                                                                                                                            ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP
                                                                                                                                                                                                                                                       LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                 DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAG
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Pred. No. 1.5e-120;
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                                                                                                                                                                                                                                                 -SRTPLLSSLSATSN----NSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAF
                                                                                          PTCLSSGFNS PALWIQKGSHQMSLDNPDYQQDFFPKE
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DQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVE HAFENLEI IRGRTKOHGOFSLAVVGLNITSLGLRSLKEISDGDVIISGNRNLCYANTINW ECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPF SVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHHNTHLCFVHTVPW | : | : | : | : | : | : | : | : | : | HFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKTVKEITGFLLIQAWPDNWTDL CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRKVCNGIGIGEFK-DTLSINATNIK CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY KKLFGTPNQKTKIMNNRAEKDCKAVNHVCNPLCSSEGCWGPEPRDCVSCQNVSRGRECVE -FAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDL 602 542 477 482 417 422 357 303 537 363 299